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OM nucleic - nucleic search, using BW model

Run on: February 4, 2005, 11:44:23 ; Search time 636 Seconds
(without alignments)
10381.095 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	221.4	5.5	4422	US-09-388-221B-1	Sequence 1, Appl1
2	221.4	5.5	4556	US-09-388-221B-9	Sequence 9, Appl1
3	220.6	5.5	4200	US-09-388-221B-3	Sequence 3, Appl1
4	220.6	5.5	4332	US-09-388-221B-5	Sequence 5, Appl1
5	220.6	5.5	4466	US-09-388-221B-11	Sequence 11, Appl1
6	183.8	4.6	1371	US-08-910-731-1	Sequence 1, Appl1
7	183.8	4.6	1371	US-08-910-731-5	Sequence 5, Appl1
8	182.4	4.5	1386	US-08-910-731-7	Sequence 7, Appl1
9	180.8	4.5	1374	US-08-910-731-3	Sequence 3, Appl1
10	175.8	4.4	1374	US-08-910-731-3	Sequence 3, Appl1
11	175.8	4.4	1374	US-08-910-731-3	Sequence 3, Appl1
12	61	1.5	7218	US-08-232-463-14	Sequence 14, Appl1
13	60	1.5	376	US-09-023-655-395	Sequence 395, App
14	51.4	1.3	64309	US-09-949-016-16600	Sequence 16600, A
15	50.8	1.3	64309	US-09-949-016-14581	Sequence 14581, A
16	47.4	1.2	4485	US-09-949-016-3209	Sequence 3209, Ap
17	47.4	1.2	4485	US-10-014-269-1	Sequence 1, Appl1
18	47.4	1.2	4485	US-10-014-269-33	Sequence 33, Appl1
19	46.6	1.2	1276	US-09-177-325-2	Sequence 2, Appl1
20	46.6	1.2	1276	US-09-411-812A-2	Sequence 2, Appl1
21	46.6	1.2	1276	US-09-590-113-2	Sequence 2, Appl1
22	46.4	1.1	2780	US-09-620-312D-358	Sequence 358, App
23	45	1.1	929	US-09-671-317-14	Sequence 14, Appl1
24	44.8	1.1	1620	US-09-134-000C-340	Sequence 340, App
25	43.4	1.1	1001	US-09-671-317-439	Sequence 439, App
26	43.2	1.1	193303	US-09-497-855A-37	Sequence 37, Appl1
27	43.2	1.1	193303	US-09-497-855A-44	Sequence 44, Appl1

28	42.8	1.1	1449	US-09-248-796A-4693	Sequence 4693, Ap
29	42.8	1.1	767677	US-09-949-016-12147	Sequence 12147, A
30	42.8	1.1	767677	US-09-949-016-17361	Sequence 17361, A
31	42.6	1.1	693	US-09-252-991A-11050	Sequence 11050, A
32	42.6	1.1	1005	US-09-252-991A-110976	Sequence 10976, A
33	42.6	1.1	1185	US-09-252-991A-11203	Sequence 11203, A
34	42.4	1.1	150394	US-09-949-016-13042	Sequence 13042, A
35	42.2	1.0	38566	US-09-949-016-15271	Sequence 15271, A
36	42.2	1.0	38566	US-09-949-016-15272	Sequence 15272, A
37	42	1.0	3117	US-09-614-221A-275	Sequence 275, App
38	41.8	1.0	7044	US-09-949-016-14113	Sequence 14113, A
39	41.6	1.0	2223	US-08-257-073-4	Sequence 4, Appl1
40	41.4	1.0	505	US-09-621-976-15639	Sequence 15639, A
41	41.2	1.0	810	US-09-614-221A-103	Sequence 103, App
42	41.2	1.0	43795	US-08-742-185-101	Sequence 101, App
43	41	1.0	505	US-09-621-976-15639	Sequence 15639, A
44	41	1.0	10391	US-09-902-540-958	Sequence 958, App
45	40.4	1.0	240157	US-09-949-016-16264	Sequence 16264, A

ALIGNMENTS

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RESULT 1
US-09-388-221B-1
; Sequence 1, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-09-388-221B-1

Query Match      5.5%; Score 221.4; DB 4; Length 4422;
Best Local Similarity 47.9%; Pred. No. 9.1e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;

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DB      1132 GTGAGTCTGCTGAGACTATCGAAGAAATGGAGACAGCATTCGGGCTTCCATTGACAG 1191

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DB      1192 ATCTGTGTAGCCAGACGCGCTCTTCACTTCATGATGTGATGAGACCGAGATGG 1251

QY      832 GTTCTCAACATGACA---CAAAGCTTGCAAAAGATGGGCTGGAAGACAGCTCCGCTTC 888
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DB      1252 GTCTTGACAGAGCCGAGTTCATGAGCTGTGTGACAGCCAGCCACACCTGGCGGAT 1311

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Db      1372  GCTGGAGCAACAGCTCTGACAGAACTCATTCCTTTTGGAGCAGGACGTTGGGTAG 1431
Qy      1009  GTTAGAGAAATCTCGGGGAAACAAAGATCCAATTGCTCTTGAACGGGGATTTGTAG 1068
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Qy      1609  CACTGCTTTGGATGAAGCGTTTCTGTTGGCCCTCGAGCGAAGATGAAGAGGCCA 1668
Db      1999  ---GGGGCATCAACACAGTTTCTTATTTGGGCTGTTAATGATGAGGGGAGAGAG 2055
Qy      1669  CTGAGAGTCTGCTGAGGCTGTCCCGTTCCTCGGGGAGTGAAGACAGAGCTTCTGCACTG 1728
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Qy      1729  GTCTCTCTGTTGGGTGACAGACCTAATGCAACAACCCAGAGACACCTTGAGCGCTTC 1788
Db      2116  TCCCTGAGCTGCTGCTGACGCC-----ACACTCTCTGGAATCCCTC 2157
Qy      1789  CACTGTCTTTTTCGAGACTCAAGACAAAGATTTGTGCTTGGCAATTAACAGCTTCCA 1848
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Qy      1849  GAAAGTGGCTTCGATTAACAGAACTGAGCTGATAGATCTTCTTCTGCTCCAG 1908
Db      2218  GAAATGGGCAATGTGTGTAAGAAACAGACATGAGCTCTTAGTGTGCACTTTTCTGCAATTA 2277
Qy      1909  CACTGTCTGATTTTTCGGAAAATTCGGGTGATGATCAAAAGGATCTTCCAAAGATGAG 1968
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Qy      2089  GGCAGCAGCATCTCGACAGAGCGGGCCATGAAGCCCTGTGTGCCAAGCTGAGGATCCC 2148
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Db      2626  GTGCTCAGGATGCTGAGGCCAAACACTTTCAGAGACTGAGACAGCCGAGCTGCAAG 2685
Qy      2326  TTGAGTCTTTGAGGCTGATGCTGTGATGATGACCCATGCGCTGTACTGAAATCTCC 2385
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Qy      2386  CAAATCTTAACAGCTTCCCGAGCGCTGAATCTCTGAGCCTGACGAGAAACAAGTACA 2445
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Db      2866  CTGGGCTTGA 2876
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RESULT 2
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-IJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(4365)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-9

Query Match      5.5%; Score 221.4; DB 4; Length 4556;
Best Local Similarity 47.9%; Pred. No. 9.3e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;
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Qy      592  ATTGGAAATTCGGTCTTAGCCAGAAAGATGCTGTGTGTGGGCGCAAGGTGACTTAC 651
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Qy 1369 GACGACTCATGTTTCAAGAGACTCGGGAGTCTGAGCTCCGCTCTGTTTCAATGAAC 1428
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Qy 1609 CACTGCGTTTGAAGAGAGCTTTCTGTGTTGGCTCGAGAGAGAGAGATGAAGAGGCA 1668
Db 1999 ---GGGAGCATACACAGCTTTCTATTTGGCCCTTTAAGTGAAGAGGAGAGAGAG 2055
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Qy 1729 GTCTCTGTGGGTCAGACAGCTTAATGCCAACACCCAGAGAGACACCTTGAGCGCTTC 1788
Db 2116 TCCCTGAGCTGCTGCTGACCC-----ACACTCTGTGAGTCCCTC 2157
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Qy 1909 CACTGTCCGTATTTGCGGAAATTCGAGGTGATGTCAAGAGGATCTTCCCAAGATGAG 1968
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Qy 1969 TCCGCTGAGGATGCTCTGTGCTCCTTATGATTCGGGATTAAGACCTCATTTAGAGAG 2028
Db 2331 AACATGAGCCCAACATGTATGCTCTGTTCAGGTGGGTCC-----CAGTCAAGATGCC 2385
Qy 2029 CAGTGGGAAATTTGTGCTCAATGTGGCAACCAACCACTCCGCACTGAGACCTG 2088
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Db 2626 GTGCTCAAGATGTGAGAGCAAAACCTTTGCCAGAGACTGAAGACCCAGCTGCAAG 2685
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Db 2866 CTGGGGCTGGA 2876

RESULT 3
US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388, 221B
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4200
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(4197)
US-09-388-221B-3

Query Match      5.5%; Score 220.6; DB 4; Length 4200;
Best Local Similarity 48.0%; Fred. No. 1.5e-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;

Qy      532 TTTGATTGAGACCGGTGGGGCTTCCGGCTCGCACGGTGTTTCCAGGAAAGTCAGAG 591
Db      952 TTTGGCCAGGCGCTGGATACCCAGAGAACTCGCATATGTCATCTGCGGGGCTGTGGA 1011
Qy      592 ATTGGAAATCGGCTCTAGCCAGAGAGATCGTGTGTCGGCGCAAGTGGACTTAC 651
Db      1012 ATTGGAAATCGCAACTGGCCAGGCGAGGTGAAGAACCTGGGGAGAGGCGCACTGTAT 1071
Qy      652 CAGGGAATGTTCTCTACGTCTTCTCTCTCCCGTTAGAGAGATGCAAGCGGAAGAGAG 711
Db      1072 GGGAGCCGCTTCAGCATGTCTTCACTTCAGCTGCAAGAGCTGCGCCAGTCCAAAGTG 1131
Qy      712 AGCAGTGCACAGAGTTTATCTCCAGGAGTGGCCAGACTCCAGGCTCGGTGACGGAG 771
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Qy      772 ATCATGTCGCCAGCAAGAAAGGCTGTTGTCATTTGACGGTTTCGATGACTTGGGCTCT 831
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Db      1552 CTGTGGCCCTGGGTGTCTGTGGCTGGCTGCACTTGCTGATGACAGATGAAGGGAG 1611
Qy      1189 GAGAGCGTGGCCCCCTTCAACCAACGCTCAAGGCTGTGACGCGCTTTTGTGTTTCAT 1248
Db      1612 GAAAAAATCAACATGACTTTCAGAGCAACCAACCTCTGTCTTACATTTACCTTGCCAG 1671
Qy      1249 CAGGTACCCCTCGAGGCGGTGCGGGCTGCTGATCAATCTGAAGAAAGATTGTCCTG 1308
Db      1672 GCTCTTCAAGCTCAGACCATGG-----GACCCAGCTTC 1704
Qy      1309 AAGCGCTTTCGCTGATGCTGTGAGAGAGATGTGGAATAGAAAGTCAGTGTGTGATGT 1368
Db      1705 AGAGACCTCTGCTCTGTGGCTGTGAGGGCATCTGGCAAAAAGAACCTTTTTCAGTCCA 1764
Qy      1369 GACGACCTCATGTGTTCAAGAACTGGGGAGTCTGAGCTCCGTGCTGTGTTCAATGAAC 1428
Db      1765 GATGACCTCAGAGAGCATGGGTATGATGGGCGCATCATCTCACCTTCTTGAAGATGGGT 1824
Qy      1429 ATCTCTTCCCAAGCAGGCACTGTGAGAGATCAACACTTCTTCCACTGATCTCCAG 1488
Db      1825 A---TTCTTCAAGAGCAACCCATCTCTGTAGCTACAGCTTCATTCATCTGTGTTTCCA 1881
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Qy      1489 GACTTCTGTGCGGCTTGTATCAAGTGTGAGGGGCTTGAAATCGACCGACTCTGTC 1548
Db      1882 GAGTTCCTTTCAGAGAAATGCTCTATGTCTTGAGAGATGAGAAAGGAGATTAACATTTCT 1941
Qy      1549 CCTCTGATGCTGAGAAACAAAGAGGTCATGAGAGCTTAAACAGGAGCTTCATATC 1608
Db      1942 AATTGCATCATATGTTTGAABAAACCTTGAAACATATGAAATATCATGCGCTTTGGG 2001
Qy      1609 CACTGCTTTGATGAAGACGTTTCTGTTGTGGCTCGTGAACGAAAGCTTAAGAGAGCCA 1668
Db      2002 GCATC-----AACCAACGTTTCTATGTGGGCTGTAAATGTATGAGGGGAGAGAGAG 2055
Qy      1669 CTGAGAGTCTGCTGGGCTGTCCCGTTCCCTCGGGGTGAAGCAAGACTTCTGACTGG 1728
Db      2056 ATGAGAGAACTTTTCACTGCGCGCTGTCTCAAGGGAGAGAACTGATGCAAGTGGTCCG 2115
Qy      1729 GTCTCTGTTGGGTGAGAGCGCTTAATGCCAACCCAGAGAGACACCTGAGAGCGCTTC 1788
Db      2116 TCCCTGAGCTGTGCTGCAAGC-----ACACTCTGTGAGTCCCTC 2157
Qy      1789 CACTGCTTTTTCAGACTCAAGCAAAAGATTGTGCTTGTGCAATTAACAGCTTCCA 1848
Db      2158 CACTGCTTTATCAGAGACTCGGAAACAAACGTTCCCTGACAAAGTATGAGGCCATTTGAA 2217
Qy      1849 GAAATGCGCTTCCGATTAACAGAACTTGAATTATGATCTTCTTCTGCTCAG 1908
Db      2218 GAAATGGGCAATGTGTATGAAGACAGATGAGCTCTTAATGTGTGCACTTCTGCAATTA 2277
Qy      1909 CACTGCTGATTTTGGGAAATTTGGGGATGATCAAGAGGATCTTCCCAAGATGAG 1968
Db      2278 TTCAAGCCGCACTGAAAGAGCTTCACTGATTAATGAGGACAG-----CAGCAAGATC 2330
Qy      1969 TCCGCTGAGGAGATGCTCTGTGTCTCTTATGAGATGCGGATTAAGACCTCATTTAGAGAG 2028
Db      2331 AAGATGAGGCCACCATGATGATCTGTTCAAGGTGG-----TCCAGTCAAGATGGC 2385
Qy      2029 CAGTGGAAATTTCTGCTCATGCTTGGCAACCAACCACTGCGGCACTGAGTGGACCTG 2088
Db      2386 TATTGGAGATTCCTTCTCCGCTCAGAGTCAACGAAACCTGAAGAGCTGGAACCTTA 2445
Qy      2089 GGCAAGCAGATCCGACAGAGCGGGCCAATGAAGCCCTGTGTGCAAGCTGAGGACATCC 2148
Db      2446 AGTGAATCTGCGAGGCACTGTGAGTAAGATTTGTGAAGACCTGAGAGCGGCT 2505
Qy      2149 ACTGCAAGATACAGACCTGATGTT---TAGAAATCAGAGATTAACCTGTGTGTCAG 2205
Db      2506 CGTGCCTCTGAGAGACCTGGCGGTTGGCTGTGGCTGTCAAGCTGAGAGACTGCAAG 2565
Qy      2206 CACTCTGAGAAATGTCATGCGCAACCGTAACTTAAGATCCTCAACTTGGAGGCAAC 2265
Db      2566 GACCTTGCTTGGGCTGAGAGGCCCAACAGACCTGACCGAGCTGAGACTGAGCTTCAAT 2625
Qy      2266 CACTGGAAGAAAGATGTAAGATGGCGGTGGAACCTTAAACCCCAAAATGTTG 2325
Db      2626 GTGCTACAGATGTGTAGGCGCAACACTTTCAGAGACTGAGACCGGAGCTGCAAG 2685
Qy      2326 TTGAGATCTTTGAGGCTGGAATGCTGTGATTAAGCCATGCTGTTACTGAAGATCTCC 2385
Db      2746 TCTGTCTTATGTGCACAGCCCAAGGCTGAAGAGCTTAAGCTGACAGCAACAACTGGAT 2805
Qy      2446 GACCAAGGAGTAATGCTCTCAATGATGCTTGAAG 2480
Db      2806 GACGTTGGCGTGCAGCTGTGTGAGGGGCTCAG 2840
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RESULT 4
US-09-388-221B-5
; Sequence 5, Application US/09388221B

Patent No. 6818750
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
FILE REFERENCES: P-LJ 3650
CURRENT APPLICATION NUMBER: US/09/388,221B
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4332
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(4332)
US-09-388-221B-5

Query Match 5.5%; Score 220.6; DB 4; Length 4332;
Best Local Similarity 48.0%; Pred. No. 1.6e-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;

QY 532 TTGATTCAGACCGGTGGGCTTCGGCTCGACGGGTGTTCTGACGGAAGTCAGGA 591
DB 952 TTGGCCAGGCTGATACCAAGAACTCGCATATGATACAGGGGGCTGTGGA 1011
QY 592 ATTGGGAATGGCTTACGCAAGATCGTCTGTCTGGGCGCAAGTGTGACTTAC 651
DB 1012 ATTGGGAAGTCAGACCTGGCAGGCGGTGAAGAGCTGGGGAGGGCAGCTGTAT 1071
QY 652 CAGGAATGTTCTCTACGTCTTCTCTCCCGTTAGAGATGACGGAAGAGAG 711
DB 1072 GGGGACCGCTTCAGCATGTCTTCTACTTCAGCTGCAAGAGCTGGCCAGTCCAGTGG 1131
QY 712 AGCAGTGCACAGATTCATCTCAAGGAGTGGCCAGCTCCAGGCTCCGTTAGCGAG 771
DB 1132 GTGAGTCTGGTGAAGCTCATCGAAAGATGGGACAGCCATCGGGCTCCATTAGACAG 1191
QY 772 ATCATGTCGCAACCAAGAGCTGTGTTCACTATGACGTTTGCATGACCTGGGCTCT 831
DB 1192 ATCTGCTTAGGCGCAAGAGCGGCTGTCTTCATCTCCAGATGTGATGAGACCGAGATGG 1251
QY 832 GTCCCAACAAATGACA---CAAGCTGTCAAGAGCTGGGCTGAGAACAGCTCCGTTTC 888
DB 1252 GTCTTTCAGAGCCGAGCTTCTGAAGCTCTGTCTGCACTGAGACCAAGCCAGCCGAT 1311
QY 889 ACCCTCATACGACAGCTGCTGAGAGAGTCTGCTCCCTGAGTCTTCTGATGCTCAC 948
DB 1312 GCATGCTGGGCAAGTTGCTGGGGAACCTATATCTTCCGAGGATCTTCTGATACG 1371
QY 949 GTCAGAGCTGGGCAAGAGAGTCAAGTCAAGTGTGTCTCCCGTTTACTGTTA 1008
DB 1372 GCTGGGACCAAGCTCTGCAAGACCTCATCTTCTTGGAGAGGCAAGTTGGGTAAG 1431
QY 1009 GTTAGAGAAATCTCCGGGGAACAAGATCACTTGTCTCTGAGCCGGGATTTGTAG 1068
DB 1432 GTCTGGGGTCTCTGAAGTCAAGCAAGGAAGATTTCTACAGATATTTTCAAGATTA 1491
QY 1069 CATCAGAAACACAGAGGTTGCTGTCATGATGAAACAAGCTGAGCTGCAACAGTGC 1128
DB 1492 AGGCAAGAAATTAGAGCTTTAGTGTCTAAATCAACAAGAGCTGTGGGCTGTGT 1551
QY 1129 CAGGTCCCGCGTGGGCTCTCTCATCTGCTGGGCTGCAAGCTGCAAGAGAGTGTGGG 1188
DB 1552 CTGTGGCTTGGGCTGTCTGCTGGGCTGCAAGCTGCAAGAGAGAGAGAG 1611
QY 1189 GAGAGCGTGGCCCTTCAACCAAGCTCAAGGCTGCAAGCGCGCTTTGTGTTTAT 1248
DB 1612 GAAAAATCTCACTGATTCAGAGCAACCAAGCTCTGTCTTACATTTACCTTGGCCAG 1671
QY 1249 CAGCTCAACCTCTCAAGGCTGGTCCGAGCTGTCTCAATCTGAGAAAGATGTCTCTG 1308
DB 1672 GCTCTCAAGCTCAGGCAATGG-----GACCCAGCTC 1704

QY 1309 AAGGCTTCTGCGCTATAGCTGTGAGGAGAGTGTGAATAGAAATCAGTGTGATG 1368
DB 1705 AGAAGCTCTCTCTCTGCTGCTGAGGGGATCTGGGAAAAAAGACCTTTTACGTCA 1764
QY 1369 GACCACTCATATGTTCAAGAGCTGGGAGTGTGAGCTCCGTCTCTTTCACTAAC 1428
DB 1765 GATGACCTCAGAGAGCATGAGGTATGATGGGCGCATCATCTCCACCTTCTTAAGATGG 1824
QY 1429 ATCTTCTCCCAAGACGACCTGAGAGATCAACCTTCTTCCACCTGATCTCAG 1488
DB 1825 A---TTCTTAAGAGCAACCCATCTCTGAGTACAGCTTCATTCACCTTGTTCAA 1881
QY 1489 GACTTCTGCGCGCTTGTACTAGTGTGAGAGGCGCTGAAATCAGACCACTCTGTC 1548
DB 1882 GAGTCTTTGACAGAAATCTCTATGTCTTGAAGATGAGAGGGAGAGATTAATCT 1941
QY 1549 CCTCTGTAAGTGAAGAACAAAGAGTCCATGAGCTTAAACAGGAGCTTCCATATC 1608
DB 1942 AATTGATCATATGATTTGAAAGAACCTGAGACATATGAAATATATGCTGTTGG 2001
QY 1609 CACTGCTTTGATGAAGAGCTTTCTTGTGGCTCTGAGCGAAGAGCTTAAGAGGCA 1668
DB 2002 GCATC-----AACCAACGTTTCTTATGAGGCTGTTAAGTGTAGAGGGGAGAGAG 2055
QY 1669 CTGAGAGTCTGCTGGGCTGCTCCGCTCCCTGGGGGGAAGAGAGAGCTTCTGCACTGG 1728
DB 2056 ATGAGAAACATTTTCACTGCGGCTGTCTAGGAGAGAACTGATGATGATGCTCCG 2115
QY 1729 GTCTCTGTGGGTGACAGAGCTTATGCAACCAACCCAGAGACAACCTGAGAGCTTC 1788
DB 2116 TCCCTGAGAGCTGCTGAGAGC-----ACACTCTGAGAGCTTC 2157
QY 1789 CACTGTCTTTTGAAGTCAAGACAAAGATTTGTGCTTGGCTTGAATTAACGTTCCA 1848
DB 2158 CACTGCTTGTACGAGTCTGAGCAAAACGTTCTGACACAAGATGAGCCATTTGCA 2217
QY 1849 GAAGTGGGCTTCCGATTAACAGAACCTGAGCTTATGATCTTCTTCTGCTCCAG 1908
DB 2218 GAATGGGATGTGTGTAAGAAAGACATGAGACTTTAGTGTGACATTTTGTGATTA 2277
QY 1909 CACTGTCCGTAATTCGGAATAATTCGGGTGATGTCAAGAGATCTTCCAGAGATGAG 1968
DB 2278 TTCAGCGGCCACGTAAGAGCTTCAAGTATTAAGGGCAGG-----CAGCACAATC 2330
QY 1969 TCCGCTGAGGATGCTCTGTGTCTCTATGATGCGGGAATGAAGCTTATGAGAG 2028
DB 2331 AACATGAGGCCCAACATGTGATGCTGTTCAGGTTGG-----TCCAGTCAAGATGCC 2385
QY 2029 CAGTGGGAATTTCTGCTCCATGCTTGGACCAACCAACCACTGGGCAAGCTGGA 2088
DB 2386 TATTGGAGATTTCTTCTCTGCTTCAAGGTCAACAGAAACCTGAGAGAGCTGAACTTA 2445
QY 2089 GGCAGACAGATCTGACAGAGCGGGCATTGAAGACCTGTGTGCAAGCTGAGGATCCC 2148
DB 2446 AGTGAAGATCTGAGAGCACTGCAAGTGAAGACTTTTGAAGCCCTTAAGAGGCTT 2505
QY 2149 ACTTGAAGATACAGACCTTGATGTT---TGAATGCAAGATTAACCTGTGTGAG 2205
DB 2506 CGTGGCTCTGAGAGACCTGCGGTGGCTGTGTGCTTCAAGCTGAGAGAGCTGCAAG 2565
QY 2206 CACTCTGAGAAATCTGATAGGCAACCTTAACCTTAAGATCCCTCAACTTGGAGGAGC 2265
DB 2566 GACCTTGGCTTGGGCTGAGAGCCCAACAGACCTTGAACGAGCTGAGACCTTCAAT 2625
QY 2266 CACTGAAGAGAGATGTAAGATGAGGCTGTGAACCTTAAACCAACCAAAATGTTTG 2325
DB 2626 GTGCTACGATGCTGAGAGCAACCTTTGCCAGAGCTGAGACAGCGGAGCTGCAAG 2685
QY 2326 TTGAGTCTTTGAGCTGAGATTTGCTGTGATTAACCAATGCTGTATCTGAAGATCTCC 2385
DB 2686 CTACAGAGCATGAGAGCTGTGAGCTGTGCTCACGTGATGCTGTGCAAGAGAGCTGAGCC 2745

Qy 2386 CAATCTTACGACCTCCCGACGCTTGAATCTTGAAGCTTGGCAGAGAAAGATGACA 2445
Db 2746 TCTGTGCTTAAGTCCAGGCCCCAGCCTTGAAGAGATGACAGCAAGAACTTGAT 2805
Qy 2446 GACCAAGGAGTAAATGCTCTCAATGATGCTTGAAG 2480
Db 2806 GACCTTGGCGTGCAGACTCTCTGTAGAGGGCTCAG 2840

RESULT 5

US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-1J 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: CDS
; LOCATION: (1) ..(4272)
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-11

Query Match 5.5%; Score 220.6; DB 4; Length 4466;
Best Local Similarity 48.0%; Pred. No. 1,66-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;
Qy 532 TTGTGATCAGACCGGTGGGGCTTCGAGCTTCGACAGGTGTTTTCGACGAGAAAGTCAGGA 591
Db 952 TTTGGCCAGGCGTGTATACCAAGAACTCGCATATCATATCTGACAGGGGCTGTGGA 1011
Qy 592 ATTGGGAAATGGCTCTTCCAGAGAGATCGTCTGTCTGGGCGCAAGTGTGACTTAC 651
Db 1012 ATTGGGAAATCAACCTGGCCAGAGGTGAAGAAAGCTGGGGAGAGCCAGCTGTAT 1071
Qy 652 CAGGAAATGTTCTCTAAGTCTTCTTCTCCCGTTAGAGAGATGACAGCGGAAGAGAG 711
Db 1072 GGGAGCGCTTCAGCATGTCTTCTTCACTTCACTGACAGAGAGCTGGCCATGCCAGGTG 1131
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Db 1432 GTCCGGGGTCTCTGAGTCCAGAGAGAAATTTTCTACAGATATTTCAAGATGAA 1491

Qy 1069 CATGAGAAACACAGAGGTCCTGTCGATCATGAACAAGCTGAGCTTCGACAGTGC 1128
Db 1492 AGGCAACAAATTAGAGCTTTAGGTTTGAATCAAAACAAAGAGCTTGGGCCCTGTGT 1551
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Db 1552 CTGTGCTCTGGGTTCTCTGGCTGGCTGACCTTGGCTGTATGACAGATGAAGCGGAG 1611
Qy 1189 GAGAGCTGCCCCCTTCAACCAACGCTCAAGGCTTCGACGCGCGCTTTGTGTTTCAT 1248
Db 1612 GAABAACTCACATGACTTCACAGACCAACCAACCTCTGTGTACATTAACCTTGCCAG 1671
Qy 1249 CAGTCAACCCCTGAGGCGGTGTCCGCGCTGTCTCATATCGAGAGAAAGTTGTCTG 1308
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Qy 1309 AAGGCTTTCGCGGTATGAGCTGTGAGAGAGTGTGAATGAAAGTCAAGTGTGATGT 1368
Db 1705 AGAAGCTCTGTCTCTGGCTGTGAGAGGCACTTGGCAAAAAGAACCTTTTCAGTCCA 1764
Qy 1369 GACGACCTCATGTTCAGAGACTCGGGAGTCTGAGCTCCGTCTGTTCACATGAAC 1428
Db 1765 GATGACCTCAGAGAGCATGGGTTAGATGGGGCCATCATCTCCACCTTGAAGATGGGT 1824
Qy 1429 ATCTTCTCCCAACAGCAGCTGTGAGAGTACTACCTTTCTTCCACCTCAAGTCTCAG 1488
Db 1825 A---TCTTCAGAGCAAGCCATCCCTCTGAGCTCAGCTTCATTCATCTCTGTTCAA 1881
Qy 1489 GACTCTGTGCGCGCTTGTACTAGTGTAGAGGGCGCTGGAATTCAGCCAGCTCTGCG 1548
Db 1882 GAGTCTTGTGAGAAATGCTTATGTCTTGAAGATGAAAGGAGAGATTAACATTTCT 1941
Qy 1549 CCTCTGTACCTTGAAGAAAGAGGTTCATGAGCTTAAACAGGAGCTTCATATTC 1608
Db 1942 AATTGCAATATAGTTTGAAGAGAGCTAGAGCATATGAAATATAGAGCTGTGGG 2001
Qy 1609 CACTGCTTTGATGAAGACGTTTCTTGTGTGGCTCTGTAGCGAAGACGTAAAGAGCCA 1668
Db 2002 GCATC-----AACCAACGTTTCTTATGTGGCTGTAAAGTATGAGGGAGAGAGAG 2055
Qy 1669 CTGAGAGTCTGCGGGCTGTCCCGTCCCTGGGGGTGAAGAGCAAGCTTTCGACATGG 1728
Db 2056 ATGGAAGAACTTTTCACTGCGGCTGTCTAGGGAGAGAACTGATGCAAGTGGTCCG 2115
Qy 1729 GTCTCTGTGTGGTTCAGAGCTTAATGCCACCAAGGAGAGCAAGCTTCAGAGCTTC 1788
Db 2116 TCCCTGAGGCTGCTGCTGAGGCC-----AACCTCTGGAGTCCCTC 2257
Qy 1789 CACTGTCTTTCGAGACTCAAGACAAAGATTGTTGCTTGGCATTAACAGCTTCCA 1848
Db 2158 CACTGCTGTATCGAGACTCGGAAACAAACGTTCTGTACAAAGTATGGCCATTTGAA 2217
Qy 1849 GAATGTGGCTTCGAGTTAACAGAACTGTGATATGATATTCCTTCTGTGCTCAG 1908
Db 2218 GAATGTGGCAATGTGTGAABAAAGACATGAGCTTTATGTGCACTTCTGTGATTA 2277
Qy 1909 CACTGCTGATTTGCGGAAATTCGGGTGATGTCAAGAGGATCTTCCCAAGATGAG 1968
Db 2278 TTGACCGCCAGCGAAGAGCTTCAAGCTATTAAGAGGAGG-----CAGCAGATC 2330
Qy 1969 TCGCTGAGGAGTCTGTGTGTCCTGTATGATGCGGATGAAGACCTCATATGAGAG 2028
Db 2331 AACATGAGAGCCCAACATGTGTAGTCCGTTCAGAGTGG-----TCCAGTACAGATGCC 2385
Qy 2029 CAGTGAAGAAATTTCTGCTCAGTCTTGGGACCAACCAACCAAGCTGGCGGAGCTGAGACTG 2088
Db 2386 TATTGGCAATTTCTTCTCTGCTCAAGGTCAACGAAACCTGAAGAGCTGAGACTTA 2445
Qy 2089 GGCAGAGCACTCTCAGAGAGCGGGCATGAGACCTGTGTGCGCAAGCTGAGGACTCCC 2148
Db 2446 AGTGAAGAACTCGCTGAGCCACTCTGCAGTGAAGATTTTGTGAAGACCTGAGAGCGCCT 2505
Qy 2149 ACTGCAAGATACAGACCTGATGTT---TAGAAATGACAGATTAACCTCTGTGTGAG 2205

Db 1062 GGAAGTGGCCAGGCGCTGAGCCAGCCGAGCAACAATGCGGTGCTCTCTTGGGA 1121
Qy 3033 ATGTGACTGACTTCTGATGCTGTGAGGCACTCTCTTGGCCCTTTCGAAACCGGCA 3092
Db 1122 CTGTGAGGTGACCAACAGCGGCTGAGAGAGCTGCGCTCTGCTGTGGCCAAACCGAG 1181
Qy 3093 TCTGACCAAGTAAACCTGTGTGAGATTAATTAAGTCCAAAGGAATGATGAAGCTGTG 3152
Db 1182 CCGTGAAGAGCTGAGCTGAGCAACAATGTGTGGGCGAACCCGGGCTGTCTGCAAGCTGCT 1241
Qy 3153 TTGGCCCTTTCGCTGTCTCCAGCTTAATCTTACAGATTAATGGGCTGTGGAATGCACTA 3212
Db 1242 GGGAGGCTGAGAGAGCCGGGCTGGCCCTGAGAGAGCTGTGCTGTACGACACTACTG 1301
Qy 3213 CCCTGTGCAATTAAGAGAGCTGTGAGAGAGAGTGAAGTCAAGCCCG 3263
Db 1302 GACGAGAGAGGTGAGAGAGCCGCTGAGAGCCCTGAGAGGAGCAAGCCCG 1352

RESULT 7

US-08-795-395-1

Sequence 1, Application US/08795395

Patent No. 5965399

GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI

TITLE OF INVENTION: Cloning and Expression of Rat Liver and

TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,395

FILING DATE: 04-FEB-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942.3440002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1371 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1368

US-08-795-395-1

Query Match 4.6%; Score 183.8; DB 2; Length 1371;

Best Local Similarity 47.2%; Pred. No. 7e-44; Indels 3; Gaps 1;

Matches 591; Conservative 0; Mismatches 657; Indels 3; Gaps 1;

2016 CCTCATGAGAGCAGTGGGAAGATTCTGCTCATGCTTGGCAACCAACCAACTCTCG 2075

Db 102 CCTACGAGAGAGAGCTGCAAGAGCAATCGGTTCTGCGCTTCGAGCAACCCCTCTGAC 161
Qy 2076 GCACTGGAACCTGGGAGAGAGCAATCTGACAGAGCGGAGCATGAAAGCCCTGTGTGCA 2135
Db 162 GAGACTCTGCTCCGACACCAAGCTGGGAGATGCCGGGCTGTGACCTGTGTGTGAGAGG 221
Qy 2136 GCTGAGGCAATCCACCTGCAAGATACAGACCTGATGTTTGAAGATCAAGATTACC- 2194
Db 222 CCTGCAAGAGCCCACTGCAAGATCCAGAAAGCTCAGCTGAGAACTGCTCCCTGACGGA 281
Qy 2195 --CTGTGTGTGAGAGACCTGTGAGAAATGCTATAGGCCAACCTTAACCTTAAGATCCCTCA 2252
Db 282 GGCAGGCTGCGGGGTCTGTCCACAGACAGCTGCGCTCTGCGCCACGCTGGGAGCTGCA 341
Qy 2253 CTGGGAGGCAACCACTGAAAGAGAGATGTAAAGATGAGCGTGTGAACCTTAACA 2312
Db 342 TCTCAGGAGCAACCACTGTGGGAGAGCGCGGCTGCGCTGTCTGTAGGGGCTCTGGA 401
Qy 2313 CCAAAATGTTTGTGAGAGCTTTGAGGCTGTGATGTGATGTAACCAATGCTGTGA 2372
Db 402 CCCCAGTGCCACTGGAAGAGCTGAGTTGAGATCTGCGCTGACGCGCCAGCTG 461
Qy 2373 CTTGAAGATCTCCAAATCTTACAGACTCCCAAGCTGAAATCTTGAAGCTTGGAG 2432
Db 462 GAGCCCTGTGCTCGGTGTCTGAGGCAAGCGGAGCTTGAAGAGCTCAAGTGAACA 521
Qy 2433 AAACAAGTGAACAAGGAGATGATGCTCTGAGTATGCTTGAAGATGCTCCAGT 2492
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Qy 2613 GGGAGCAAGAGGTGAATTAATTAATCTGATGATCAATGAGGCTTCCCACTGTATCTGCA 2672
Db 702 GGGAGAGCGGAGCAATGAGCCAGCTGTGCTCCGAGCTTGAAGCCCGCTCCGCTCA 761
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Qy 3093 TCTGACCAAGTAAACCTGTGTGAGATTAATTAAGTCCAAAGGAATGATGAAGCTGTG 3152

Dh 1182 CCGGAGAGCTGAGCTGAGCAACATGCTGTGGCGACCCGGGCTCTGACCTGCT 1241
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Db 1242 GGGGAGCTTGAGAGCAGCCGGGCTGGCCCTGAGAGCAGCTGTCTCTTACGACACTTACTG 1301
Qy 3213 CCCTGTGCAATTAAGAACTGCTGAGAGAAATGAGTACTTCAACCCCG 3263
Db 1302 GACGAGAGAGGTGAGAGACCGCTCTGACAGCCCTGAGGGGAGCAAGCCCG 1352

RESULT 8

US-08-910-731-5
Sequence 5, Application US/08910731
Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,731

FILING DATE: (Herein)

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,395

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/794,546

FILING DATE: 03-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942,3440003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1386 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-08-910-731-5

Query Match 4.5%; Score 182.4; DB 2; Length 1386;

Best Local Similarity 47.1%; Pred. No. 1.9e-43;

Matches 595; Conservative 0; Mismatches 666; Indels 3; Gaps 1;

Qy 2000 GGATGCGGATTAAGACCTCTATTGAGAGCAGTGGGAGATTTCTGCTCAATGCTTGGCA 2059
Db 101 GCGTGAAGACTGTGGCTTCAAGAGACCGGTGCAAGACATGCTCTGCACTTGGAG 160
Qy 2060 CCACCCACACCTTGGCGGAGCTGGAAGCTGGGAGAGAGATCTTGAAGAGCGGAGCATGA 2119
Db 161 TCAACCTGCACTGGCAGAGCTCAACCTGCGCAGCAAGAGCTGGGCGATGTGCGCGTGC 220

Qy 2120 AGACCTGTGTGTCAGAGCTGAGGATCCACCTGACAGATACAGACCTGATGTTTGA 2179
Db 221 ATTGCTGTCTCAGAGGCTCTGACAGACCCCTCTGTGAAGATCCAGAGAGCTCCAGA 280
Qy 2180 ATGCAACATTAACC--CTGTGTGACAGACCTTGTGAAGATGTCATGTGCGCAACGTA 2236
Db 281 ACTGTGTCTGACAGGAGGCGGCGGCTGTGCTGTGACAGACACTGACACCTGTGCCA 340
Qy 2237 ACCTTAAGATCCCTCAACTTGGGAGGCAACCACTGAAAGAGAGATGTAAGATGAGGT 2296
Db 341 CCTGTGACAGAGCTGACCTTCAAGCAGACACTTGTGGGAGATGCGGCTGTGACGTCT 400
Qy 2297 GTGAAGCTTAAACCAACCAAAATGTTTGTGAGTCTTTGAGCTGTGATGCTGTGAT 2356
Db 401 GGAAGAGACTCTGGAACCCAGAGTCCGCTGGAAGAGCTGAGAGATGTCAGACC 460
Qy 2357 TGAACCATGCTGTGATCTGGAAGATCTCCAAATCTTACGACCTTCCCGAGCTGAAT 2416
Db 461 TCTGCGCTGCAAGCTGACAGGCGGCTGTGCTGCTGCTGAGGCGCAAGCTTCAAG 520
Qy 2417 CTGTGAGCTGAGCAAGAAACAGGTGACAGACAGGAGTATGCTCTCACTGATGCT 2476
Db 521 AGCTCAAGTTAGCAACACACATCATATGAGCTGAGCTGCGTCCGTGTCTGTGCCAG 580
Qy 2477 TGAAGTCTCCAGTGCAGCTGAGAGCTGATTAAGTGAAGAGCTGTGAGCAACAGCA 2536
Db 581 TGAAGACTTCCCTGCTGAGTGAAGGCTCAAGCTGAGAGCTGTGATGATCATG 640
Qy 2537 CGGTTGCAAGTGTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2596
Db 641 ACAACTGCGGAGACCTGTGCGGAGATTTGTGCTTCAAGCTTCAAGCTTCAAGCT 700
Qy 2597 TATCCAAAGACCTGAGGAGACAGAGGTGAATCTATCTGTGATTCATGAGGCTTC 2656
Db 701 TGGGAGAGAAAGCTGTGTGATGTGGGAGAGGAGCTGTGCTGAGGCTGTCCACC 760
Qy 2657 CCCACTGTAGTCTGAGAGCTGATGCTGAATCACTGAGCAACCTGAGCAACGCTGTG 2716
Db 761 CCAAGTCCAGGCTAGAGACCTGTGATCTGTGAGTGTGATCATCTGCAAGGCTGTG 820
Qy 2717 GTTTCTTGAAGCTGTGAGGTTAAGGTGAATCTGATGCTGATGCTGATGCTGATG 2776
Db 821 GGGATCTGTGCTGTGTCTTCAAGGAGGAGAGAGCTGATGAGAGCTGAGCTGTG 880
Qy 2777 ACCCTGTGAGAGCAATGTGCTGAGCTTGTGTGAGAGTATGAGAGCAATCTTGT 2836
Db 881 ACGAGCTGTGAGAGTGTGAGGCTGAGCTGTGTGTGAGACCTGTGTGAGACCTGTG 940
Qy 2837 ATCTCAGAGACCTGAGTGTGTAAGGTGATCTCAACGCGCGCTGTGTGAGAGTGT 2896
Db 941 AGCTGAGTGTGCTGTGTGTAAGTCTGTGAGCTTCAAGCGCTGTGCTGCTGCTTCA 1000
Qy 2897 CCTGTGTGATCTGAGAGAGAGCAACCTGAAAGAGCTGTGATCTCAAGCAATGTG 2956
Db 1001 GCTGAGTGTGCTGAGAGAGAGGTTTCTTGTGAGCTTCAAGTAAAGCAACAGGCTG 1060
Qy 2957 GTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3016
Db 1061 AGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
Qy 3017 GACTGAGTGTGAGAGCAATGTGAGCTGCTGATGCTGATGCTGATGCTGCTGCTGCTG 3076
Db 1121 TGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1180
Qy 3077 TTTCTGCAACCGGATCTGACAGCTTAACTGTGAGCAAGATTAATTAAGTCCCAAG 3136
Db 1181 TGTGTGCAACCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
Qy 3137 GAATGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3196
Db 1241 GCATCTGTGAGCTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
Qy 3197 TGTGAAATGCAAGTACCTGTGCAAAATTAAGAGAGCTGTGAGAGAGTGTGCACTCA 3256

Db 1301 TGTACGATTTACTGTCTGAGAGATGAGAGACCGGCTGAGGCTCTGAGAGAGACA 1360
QY 3257 AGCC 3260
Db 1361 AGCC 1364

RESULT 9

US-08-910-731-7
Sequence 7, Application US/08910731
Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,731

FILING DATE: (Herewith)

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,395

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/794,546

FILING DATE: 03-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942,3440003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1371 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-08-910-731-7

Query March

Best Local Similarity 4.5%; Score 180.8; DB 2; Length 1371;

Matches 588; Conservative 0; Mismatches 657; Indels 3; Gaps 1;

Db 2016 CCTATTGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2075

Db 102 CTTCAAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 161

QY 2076 GCAAGTGAAGCTGGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2135

Db 162 GCAAGTGAAGCTGGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 221

QY 2136 GCTGAGAGATCCCACTGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2194

Db 222 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 281

QY 2195 --CTGTGTGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2252

Db 282 GCGGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 341

QY 2253 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2312

Db 342 TCTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 401

QY 2313 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2372

Db 402 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 461

QY 2373 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2432

Db 462 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 521

QY 2433 AATGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2492

Db 522 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 581

QY 2493 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2552

Db 582 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 641

QY 2553 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2612

Db 642 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 701

QY 2613 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2672

Db 702 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 761

QY 2673 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2732

Db 762 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 821

QY 2733 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2792

Db 822 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 881

QY 2793 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2852

Db 882 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 941

QY 2853 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2912

Db 942 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1001

QY 2913 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2972

Db 1002 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1061

QY 2973 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 3032

Db 1062 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1121

QY 3033 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 3092

Db 1122 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1181

QY 3093 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 3152

Db 1182 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1241

QY 3153 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 3212

Db 1242 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1301

QY 3213 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 3260

Db 1302 CTTGAGAGAGAGAGATGAGAGAGATTCTGCTCCATGCTTGAGACCCACCCACCTGCG 1349

RESULT 10
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/795,395
; PRIORITY APPLICATION DATA:
; FILING DATE: 04-FEB-1997
; PRIORITY APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIORITY APPLICATION DATA:
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-910-731-3

Query Match 4.4%; Score 175.8; DB 2; Length 1374;
Best Local Similarity 47.2%; Pred. No. 1.7e-41;
Matches 568; Conservative 0; Mismatches 632; Indels 3; Gaps 1;

QY 2000 GGATCGGGGATTAAGACCTCATTTGAGAGCAGTGGGAGATTCTGCTCATGCTTGGA 2059
DB 86 GGCTGGATGACGTGGGCTCCTCATGTAAGTGGGAGAAAGATCAAGTCAAGATCCAG 145
QY 2060 CCCACCCACACCTGCGGACGCTGAGACCTGGGACGACATCTTGACAGAGCGGGCCATGA 2119
DB 146 CCACCCCTGCTGACAGAGCTCAAGCTACGACCAATGACTGGGTGATGCTGTGTGG 205
QY 2120 AGACCTGTGTGCAAGCTGAGGACATCCACCTGCAAGATACAGACCCGTATGTAGAA 2179
DB 206 GTCTGTGTCTCCAGAGGCTGCAAGATCCCATTTGTAAGATCCAGAGCTGAGGCTTCAG 265
QY 2180 ATGCAAGATTACCC---CTGTGTGTGCAAGACCTCTGAGAAATGCTCATGAGCCCAACGTA 2236
DB 266 ACTGCAAGCTTACGAGAGCTGTGGGTCTGTGCTGATGATGCTGAGGCTCTTTGTCTTA 325

QY 2237 ACCTAAGATCCCTCAACTTGGAGGACCCACCTGAAGAGAGATGTAAAGATGGCT 2296
DB 326 CCTGTGGAACTACATATCATATGACCAACCTCTGGGGGATGAAGGCTGAAGCTGTCT 385
QY 2297 GTGAAGCCTTAAACACCCAAATGTTGTGAGTCTTTGAGGCTGATTCCTGTGAT 2356
DB 386 GTGAAGGACTCCGGAGACCCCGAGTCCCTGTGAAAGGCTTCAAGTTGAATACTGTACC 445
QY 2357 TGACCATGCGCTGTACCTGAAGATCTCCCAATCCTTACGACCTCCCGACCTGAAT 2416
DB 446 TCAAGCTACAGCTGCGAGCCCTGGGCTTCACTGCTTCAAGGTGAACCTGACTTTAAG 505
QY 2417 CTCTAGCTGCGACAGAAACAGGTGACAGACAGAGAGTAATGCTCTCACTGATGCTT 2476
DB 506 AGCTAGTATGTAGCAACATATGATCTTCATGAGGCTGTATCAACATCTGTGCCAGGGCC 565
QY 2477 TGAAGTCTCCAGTGGCCCTGCAAGAGCTGATATCTGAGGACGTGTGACATCAAGCCA 2536
DB 566 TGAAGGATTTCTGCTGCAACTGAGTCACTCAAACTGGAGAACTGTGGTATCAATCAG 625
QY 2537 CGGCTTGCAGAGTCTGGCTCAAGCCCTCTGAGAAACCGAGCTTGAACACCTGTGCC 2596
DB 626 CCAACTGCAAGGATGTGTGTGATGTTGGGCTTCAAAAGCTCACTGCAAGAACTGAGT 685
QY 2597 TATCCAAACAAGCCTGGGGAACGAAGGTGTAATCTACTGTGTGATCAATGAAGCTTC 2656
DB 686 TGGGACGACAAAGCTGGGCAACAGAGCATTTGACAGACTGTGCTCAAGACTGTGCTTC 745
QY 2657 CCCACTGATGTGCAAGAGCTGATGTCAATCACTGACCACCTGACACGCTGCTGTG 2716
DB 746 CCAAGCTGAGGCTGAGACTGTGGCTCTGGGACTGTGATGTCACTGACAGAGGCTGCA 805
QY 2717 GTTTCTTGCACTTGGCTTAATGAGTAATCAATGCTGACGACCTGAGGCTTACATTA 2776
DB 806 AGAAGCTGTGCGGTCTCTCAAGAGCAAGCAGAGCTTAAGAACTCAAGCTTACGCTGCA 865
QY 2777 ACCCTGGGAAGACATGAGCGCTGAGACTTCTGTGCGAGGTCAATGAGAGAACATCTTGC 2836
DB 866 ATGAGCTGAAGATGAGGGTGCCTCACTGCTGTGTGAGAGCCTGTTAAGCCTGTGCTGC 925
QY 2837 ATCTCAGAGACTGAGTGTGTAAGGTATCATCTCAACGCGCGTGTGTGAGAGTCTGT 2896
DB 926 AGCTGAGTCACTGTGGGTAAAGACCTGTAGCTTCAAGCTCTCTTGTCCCACTTCT 985
QY 2897 CTTGTGTATCTGAGAGACAGACACTGAAAGCCTGATTTACGACATATGCCCTG 2956
DB 986 GCTCGGTGTGACCAAAAAGATTCTGTGTGAGTTGCAATGACAGCAACCGCTG 1045
QY 2957 GTGACGGTGGGTGTGCTGCGCTGTGCGAGGAGCTGAAGCAAAAAGAGTTCAGAGA 3016
DB 1046 GAGACTTCGAGAGTCTGTGAGCTTTCAGAGGCTTGGGCTATCCGACACAGTGTGCTG 1105
QY 3017 GACTCGGTTGAGGACATGTGACATGACTTGTGATGTGCTGAGGACATCTCTTGGGCC 3076
DB 1106 TGTCTTGTGTGAGAACTGTATATGTGACAGACAGTGGCTGACAGCCTTGGCACTGTGC 1165
QY 3077 TTTCTGCAACCGGACATCTGACCACTTAACTGTGTGCAATTAATCTTCAATGCCAAG 3136
DB 1166 TGTCTGCAACCGGACCTTGAAGGAACTGACACTGTGATTAACAACCTGAGTGGGGAACAG 1225
QY 3137 GAATGATGAAGTGTGTGTGCGCTTGTGCTGTGCTGCTGCAAGCTTAACTTACAGATTA 3196
DB 1226 GTGTCTTCAACTGTGAGAGGCTTCAAAACGCGAGCTGATCTTTCAGAGCTTGTCC 1285
QY 3197 TGT 3199
DB 1286 TGT 1288

RESULT 11
US-08-795-395-3
; Sequence 3, Application US/08795395


```

STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 636-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29t-F18
US-08-232-463-14

Query Match
Best Local Similarity 1.5%; Score 61; DB 1; Length 7218;
Matches 4; Conservative 225; Mismatches 130; Indels 0; Gaps 0;

QY 264 GAGAGAGCAGCGATGACATGAAATTTCAACACTATGAAACAGAGGTGCAC 323
D 1221 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1362
QY 324 AGCAGCAGACAGAAACAGAAATTTCAACACTATGAAACAGAGGTGCAC 383
D 1361 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1302
QY 384 AGCAGACAGAGAAACAGAGCATGAGTGACATGAGCACTACAGAGTCAGTAT 443
D 1301 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1242
QY 444 GACCAATTCCTGAGAGAGAGATGATGCTGATTTGAAAACTGCTGCTGACTG 503
D 1241 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1182
QY 504 GCCGAAATTCAGAACTGCTGCTGCTTTGATTCAGACCGGTGGGGCTTCGGCTTCG 563
D 1181 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1122
QY 564 CACGCTGCTTCAGACGGAAGTCAAGAAATTCGCAATTCAGCAGCAAGAGATCG 622
D 1121 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1063

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RESULT 13
 US-09-023-655-395
 ; Sequence 395; Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocke, Benjamin G.
 ; APPLICANT: Susan G. Stuart

```

APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 395:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLPB02
CLONE: 153338
US-09-023-655-395

Query Match
Best Local Similarity 1.5%; Score 60; DB 4; Length 376;
Matches 134; Conservative 0; Mismatches 106; Indels 1; Gaps 1;

QY 2914 AGCAGACACTGTAAGAGCTGATCTCAACGACATGCCCTGGGTGACGCTGGGGTGGCT 2973
D 35 ACCAAGAGCTGTTGAGAGCTGACCTGAGTGAACAACGCCCTCGGTGACTTGGATCAGA 94
QY 2974 GCGCTGCGAGGAGCTGAAGCAAAAGACAGTGTCTGACGAGACTCGGGTTGAAGCA 3033
D 95 CTTCGTGTGTGGGACCTGAAGCACCTGTGTGCAATCGAAGAAAGCTCTGCTGTGTCAGC 154
QY 3034 TGTGACACTGCTTGTGATGCTGTGTCGCACTCTCTTGCGCCCTTCTCGAACCGGAT 3093
D 155 TGTGCTCATCATGAGATGTTGACAGATTTTTCATCAGATTGAGACACAGCCATTCC 214
QY 3094 CTGACAG-TCTAACTGTGTGACAGAAATTAATTGAGTCCCAAGAAATGATGAGCTGTG 3152
D 215 CTGACCAAGACTCTATGTGGGGAGAAATGCTTGGGAGACTCAGAGATCGCAATTTTATG 274
QY 3153 T 3153
D 275 T 275

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RESULT 14
 US-09-949-016-16600
 ; Sequence 16600; Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 16600
;; LENGTH: 298336
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(298336)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16600

Query Match 1.3%; Score 51.4; DB 4; Length 298336;
Best Local Similarity 58.0%; Pred. No. 0.011;
Matches 91; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Oy 3273 TGACGGTAGTGGGCTCTTTTGATGAAGACGACACAAATAGGACTTACTTTCCG 3332
Db 202167 TTAGAGATGTGTGATTTATTATTTCATTCAGTACGACACAAAGTATGTTGGCATTTCC 202226
Oy 3333 GCTCCCTGAAGCCGGGATGCGCTTGTGCTGTGGGGATGAACCGAGACAGAA 3392
Db 202227 ATTCTATACATTAAAGATGCGCATGTACTGTCTGTCAATGAATCATGAAGAA 202286
Oy 3393 GAAGCGTGTGCTTGTGCTGAGACTTCAAGAGC 3429
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 14581
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(64309)
; OTHER INFORMATION: n = A,T,C or G
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Query Match 1.3%; Score 50.8; DB 4; Length 64309;
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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4035	100.0	4035	US-10-066-521-5	Sequence 5, Appl1
3	3166.2	78.5	3885	US-10-860-761-3	Sequence 3, Appl1
4	3166.2	78.5	3900	US-10-399-443-23	Sequence 23, Appl1
5	3166.2	78.5	3900	US-10-677-943-23	Sequence 23, Appl1
6	3133.6	77.7	3830	US-10-216-645-3	Sequence 3, Appl1
7	3133.6	77.7	3489	US-10-416-642-3	Sequence 3, Appl1
8	3133.6	77.7	3926	US-10-216-645-1	Sequence 1, Appl1
9	2900.6	71.9	3226	US-10-092-900A-347	Sequence 347, Appl1
10	1278	31.7	3447	US-10-399-443-5	Sequence 5, Appl1
11	1278	31.7	3447	US-10-677-943-5	Sequence 5, Appl1

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26	419.2	10.4	2575	9 <th>US-09-848-035-7</th> <th>Sequence 7, Appl1</th>	US-09-848-035-7	Sequence 7, Appl1
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28	419.2	10.4	2883	17 <th>US-10-161-493-3</th> <th>Sequence 3, Appl1</th>	US-10-161-493-3	Sequence 3, Appl1
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43	381.4	9.1	3431	16 <th>US-10-132-667-1</th> <th>Sequence 16, Appl1</th>	US-10-132-667-1	Sequence 16, Appl1
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ALIGNMENTS

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; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4035; Conservative 0; Mismatches 0; Gaps 0;

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Qy 3421 TTCAAGACAGTACCAATTTGCCAAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3421 TTCAAGACAGTACCAATTTGCCAAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Qy 3481 CAGAGATTGACCAAGTGAAGAGCTCCCGCAACCAATGCGAGCAACGAAACAA 3540
Db 3481 CAGAGATTGACCAAGTGAAGAGCTCCCGCAACCAATGCGAGCAACGAAACAA 3540
Qy 3541 CAGATTAATATGTTGATGTTGATTAATCCGAGCTGTGTGAAATGCTGAGCTGAA 3600
Db 3541 CAGATTAATATGTTGATGTTGATTAATCCGAGCTGTGTGAAATGCTGAGCTGAA 3600
Qy 3601 GGGCTTGAATCCAAAGTGTGATTAATGAACCAAGAGTAAAGCTGTGCTGAGAG 3660
Db 3601 GGGCTTGAATCCAAAGTGTGATTAATGAACCAAGAGTAAAGCTGTGCTGAGAG 3660
Qy 3661 GAGCTGAGCTGAGGGGCTGTGTGTCACAGTGTGATGACCAAGCGTGTGCTGAGT 3720
Db 3661 GAGCTGAGCTGAGGGGCTGTGTGTCACAGTGTGATGACCAAGCGTGTGCTGAGT 3720
Qy 3721 CACTGGAAGCGCTGTGCTGATGAGGCTGTGTCTTAAACAGTGTGATGACCAAGCGT 3780
Db 3721 CACTGGAAGCGCTGTGCTGATGAGGCTGTGTCTTAAACAGTGTGATGACCAAGCGT 3780
Qy 3781 GTGTCTGTGATCACTGGAAGCGCTGTGCTGATGAGGCTGTGTCTTAAACAGTGTGAT 3840
Db 3781 GTGTCTGTGATCACTGGAAGCGCTGTGCTGATGAGGCTGTGTCTTAAACAGTGTGAT 3840
Qy 3841 CACAGCGTGTGAGCTGTGCTGATGAGGCTGTGCTGATGAGGCTGTGTCTTAAACAGT 3900
Db 3841 CACAGCGTGTGAGCTGTGCTGATGAGGCTGTGCTGATGAGGCTGTGTCTTAAACAGT 3900
Qy 3901 GCTGATGACCAAGCGTGTGTCTGCTGATGAGGCTGTGCTGATGAGGCTGTGTG 3960
Db 3901 GCTGATGACCAAGCGTGTGTCTGCTGATGAGGCTGTGCTGATGAGGCTGTGTG 3960
Qy 3961 TCCAACAGTGTGATGACCAAGCGTGTGTCTGCTGATGAGGCTGTGTG 4020
Db 3961 TCCAACAGTGTGATGACCAAGCGTGTGTCTGCTGATGAGGCTGTGTG 4020
Qy 4021 GGGCTGTGTCTTAA 4035
Db 4021 GGGCTGTGTCTTAA 4035

RESULT 2
US-10-066-521-5
; Sequence 5, Application US/1006521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-334001
; CURRENT FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5
LENGTH: 4035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(4032)
US-10-066-521-5

Query Match 100.0%; Score 4035; DB 14; Length 4035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAGACAAATCGCTCACTTTTCAGCTACGGGCTGCAATGGTGTCTATAG 60
DB 1 ATGAGAGAGACAAATCGCTCACTTTTCAGCTACGGGCTGCAATGGTGTCTATAG 60
QY 61 CTAGCAGAGAAATTTCAAGCATTCAGAAATTAAGAAATTTCAAGATCG 120
DB 61 CTAGCAGAGAAATTTCAAGCATTCAGAAATTAAGAAATTTCAAGATCG 120
QY 121 ACCACATGCTCTATTCACAGATTGAAATCGAATGCAACGTGAATGTCTGCACTC 180
DB 121 ACCACATGCTCTATTCACAGATTGAAATCGAATGCAACGTGAATGTCTGCACTC 180
QY 181 CTCTTGATGATATTATGAGCATCGCTGGCTGGCTGAGTCAATGCAATCTTTGAA 240
DB 181 CTCTTGATGATATTATGAGCATCGCTGGCTGGCTGAGTCAATGCAATCTTTGAA 240
QY 241 AACATGAACCTGCGAACCCTCTCGGAGAAAGGCAAGGATGACATGAAAAAATTTCA 300
DB 241 AACATGAACCTGCGAACCCTCTCGGAGAAAGGCAAGGATGACATGAAAAAATTTCA 300
QY 301 GCTATGAAACAAGAGGTGCCACAGCAGACAGACAGAAATTTCAAGAACT 360
DB 301 GCTATGAAACAAGAGGTGCCACAGCAGACAGACAGAAATTTCAAGAACT 360
QY 361 ATGGAACAAGAGGTGCCACAGCAGACAGACAGAAATTTCAAGAGTGAACA 420
DB 361 ATGGAACAAGAGGTGCCACAGCAGACAGACAGAAATTTCAAGAGTGAACA 420
QY 421 TGGGATCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGATGACGTGATG 480
DB 421 TGGGATCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGATGACGTGATG 480
QY 481 TTTGAAAAACATGCTGCTGACCTGCCGGAATGCAAGTGGCTGTCTTTGATTC 540
DB 481 TTTGAAAAACATGCTGCTGACCTGCCGGAATGCAAGTGGCTGTCTTTGATTC 540
QY 541 GACCGGTGGGCTTCCGGCTTCGACCGGTGTTCTGACCGGAAATGCAAGTGGGAAA 600
DB 541 GACCGGTGGGCTTCCGGCTTCGACCGGTGTTCTGACCGGAAATGCAAGTGGGAAA 600
QY 601 TCGGCTCAAGCAGAGATGCTGCTGCTGGGCGCAAGGTGACCTTACCAAGGAAATG 660
DB 601 TCGGCTCAAGCAGAGATGCTGCTGCTGGGCGCAAGGTGACCTTACCAAGGAAATG 660
QY 661 TTCTCTACGCTTCTTCTCCCGTTAGAGATGACGCGGAAGAAGAGAGAGCTGTC 720
DB 661 TTCTCTACGCTTCTTCTCCCGTTAGAGATGACGCGGAAGAAGAGAGAGCTGTC 720
QY 721 ACAGAGTTCATCTCAGGGAAGTGGCAGACTCCAGGCTCCGAGTACGGAATGATGCC 780
DB 721 ACAGAGTTCATCTCAGGGAAGTGGCAGACTCCAGGCTCCGAGTACGGAATGATGCC 780
QY 781 CGACCAAGAAAGGCTGTGTTCAATGACGTTTCAGATGACCTGGGCTGTCTCTCAAC 840
DB 781 CGACCAAGAAAGGCTGTGTTCAATGACGTTTCAGATGACCTGGGCTGTCTCTCAAC 840
QY 841 AATGACAAAGCTCTGCAAGAGCTGGGCTGAGAGAGCTCCGTTCAACCTCAAGC 900
DB 841 AATGACAAAGCTCTGCAAGAGCTGGGCTGAGAGAGCTCCGTTCAACCTCAAGC 900

QY 901 AGTCTGTGAGAGAGGTCCTGCTCCCTGAGGCTTCCCTGATCCGTCACCGTCAAGAGCTG 960
DB 901 AGTCTGTGAGAGAGGTCCTGCTCCCTGAGGCTTCCCTGATCCGTCACCGTCAAGAGCTG 960
QY 961 GGACACAGAGAGCTCAAGTCAAGAGTGTGTCTCCCGTTACCTGTTAGTGAAGATC 1020
DB 961 GGACACAGAGAGCTCAAGTCAAGAGTGTGTCTCCCGTTACCTGTTAGTGAAGATC 1020
QY 1021 TCCGGGAAACAAGATTCACCTTCTCTTGAAGCGCGGATTTGGTGAACATCAAGACA 1080
DB 1021 TCCGGGAAACAAGATTCACCTTCTCTTGAAGCGCGGATTTGGTGAACATCAAGACA 1080
QY 1081 CAAGGTTGCGTGGATCAAGAACACCGGAGTGTCCACGACGATCCAGGTGCGCGCC 1140
DB 1081 CAAGGTTGCGTGGATCAAGAACACCGGAGTGTCCACGACGATCCAGGTGCGCGCC 1140
QY 1141 GTGGGCTCTCTCATCTGCGTGGCCCTTCAAGTGAAGACGTGGGGGAGAGCTGCGC 1200
DB 1141 GTGGGCTCTCTCATCTGCGTGGCCCTTCAAGTGAAGACGTGGGGGAGAGCTGCGC 1200
QY 1201 CCTTCAACCAAGCTTCAAGGCTGCAAGGCTGCAAGCGCTTGTGTTCAATCAGCTCACCCCT 1260
DB 1201 CCTTCAACCAAGCTTCAAGGCTGCAAGGCTGCAAGCGCTTGTGTTCAATCAGCTCACCCCT 1260
QY 1261 CGAGCGGTGCTCCGCGCTGTCTCAATCTGAGAGAAAGATGTCGGAAGCGCTTGC 1320
DB 1261 CGAGCGGTGCTCCGCGCTGTCTCAATCTGAGAGAAAGATGTCGGAAGCGCTTGC 1320
QY 1321 CGATGCTGTGAGAGAGTGTGAATGAGAGTCAATGTTTGAATGATGAGAGAGCTCATG 1380
DB 1321 CGATGCTGTGAGAGAGTGTGAATGAGAGTCAATGTTTGAATGATGAGAGAGCTCATG 1380
QY 1381 GTTCAAGAGCTCGGGAAGTCTGAGCTCGTCTGTTTCAATGAATCATCTTCTCCCA 1440
DB 1381 GTTCAAGAGCTCGGGAAGTCTGAGCTCGTCTGTTTCAATGAATCATCTTCTCCCA 1440
QY 1441 GACAGCCATGTGAGAGATCACTCTTCCACCTCACTCTCCAGAGCTTGTGCGC 1500
DB 1441 GACAGCCATGTGAGAGATCACTCTTCCACCTCACTCTCCAGAGCTTGTGCGC 1500
QY 1501 GCTTGTACTACGATTAAGAGGCTGGAATTCAGAGCAGGCTCTGACCTCTGACGTT 1560
DB 1501 GCTTGTACTACGATTAAGAGGCTGGAATTCAGAGCAGGCTCTGACCTCTGACGTT 1560
QY 1561 GAGAAACAAGAGTCAATGAGCTTAAACAGGCAAGCTTCAATCACTGCTTGG 1620
DB 1561 GAGAAACAAGAGTCAATGAGCTTAAACAGGCAAGCTTCAATCACTGCTTGG 1620
QY 1621 ATGAAGCTTCTTGTGCTGTGAGCGAACAATGAAGAGGCACTGGAAGTCTG 1680
DB 1621 ATGAAGCTTCTTGTGCTGTGAGCGAACAATGAAGAGGCACTGGAAGTCTG 1680
QY 1681 CTGGGCTGTCCGTTCCCTGGGGGTGAAGCAAGCTTCTGACCTGGGCTCTCTGTTG 1740
DB 1681 CTGGGCTGTCCGTTCCCTGGGGGTGAAGCAAGCTTCTGACCTGGGCTCTCTGTTG 1740
QY 1741 GGTCAAGACCTTAATGCAACCAACCAAGAGACAACCTGACGCGCTTCACTGTCTTTC 1800
DB 1741 GGTCAAGACCTTAATGCAACCAACCAAGAGACAACCTGACGCGCTTCACTGTCTTTC 1800
QY 1801 GAGACTCAAGCAAGAGTGTGCTGTGCAATTAACAGCTTCCAGAGAGTGTGCTT 1860
DB 1801 GAGACTCAAGCAAGAGTGTGCTGTGCAATTAACAGCTTCCAGAGAGTGTGCTT 1860
QY 1861 CGGATTAACCAAGACTGGAATTGATGACATCTTCTGCGCTCAAGCACTGTCCGAT 1920
DB 1861 CGGATTAACCAAGACTGGAATTGATGACATCTTCTGCGCTCAAGCACTGTCCGAT 1920
QY 1921 TTGGGAAAAATTCGGGTGATGTCAAGAGGATCTTCCAGAGATGATGCTCGCTGAGCA 1980
DB 1921 TTGGGAAAAATTCGGGTGATGTCAAGAGGATCTTCCAGAGATGATGCTCGCTGAGCA 1980
QY 1981 TGTCTGTGTCTCTATGAGATGCGGATTAAGACCTCATTTGAGAGCACTGGGAAT 2040

Db 1981 TGTCTGTGTCCTCTATGATGCGGATAGACCTCATATGAGAGAGGAGAAAT 2040
 Qy 2041 TTCTGCTCATGCTTGGGACCCACACCGGCGAGCTGAGCTGGGAGAGCATC 2100
 Db 2041 TTCTGCTCATGCTTGGGACCCACACCGGCGAGCTGAGCTGGGAGAGCATC 2100
 Qy 2101 CTGACAGAGCGGCGCATGAGAACCTGTGTGCAAGCTGAGCATCCCACTGCAAGTA 2160
 Db 2101 CTGACAGAGCGGCGCATGAGAACCTGTGTGCAAGCTGAGCATCCCACTGCAAGTA 2160
 Qy 2161 CAGACCTGATGTTTGAAGATGACAGATTAACCTGTGTGAGCACTCTGAGAAATC 2220
 Db 2161 CAGACCTGATGTTTGAAGATGACAGATTAACCTGTGTGAGCACTCTGAGAAATC 2220
 Qy 2221 GTCATGCGCAACCGTAACTTAAAGATCCCTCACTTGGAGAGCACTCACTGAGAGAG 2280
 Db 2221 GTCATGCGCAACCGTAACTTAAAGATCCCTCACTTGGAGAGCACTCACTGAGAGAG 2280
 Qy 2281 GATGTAAGATGAGCTGTGAAGCTTAAACACCCAAATGTTTGTGAGCTTTGAGG 2340
 Db 2281 GATGTAAGATGAGCTGTGAAGCTTAAACACCCAAATGTTTGTGAGCTTTGAGG 2340
 Qy 2341 CTGATGTCGTGTGATGACCCATGCTGTATCTGAAAGATCTCCCAATCTTACGACC 2400
 Db 2341 CTGATGTCGTGTGATGACCCATGCTGTATCTGAAAGATCTCCCAATCTTACGACC 2400
 Qy 2401 TCCCCAGCTGAAATCTCTGAGCTGTGAGAGAACAGGTGACAGACAGGAGATATG 2460
 Db 2401 TCCCCAGCTGAAATCTCTGAGCTGTGAGAGAACAGGTGACAGACAGGAGATATG 2460
 Qy 2461 CCTCTCAGTGAATGCTGTGAGAGTCTCCAGTGCCTGAGAGCTGATCTGAGAGAC 2520
 Db 2461 CCTCTCAGTGAATGCTGTGAGAGTCTCCAGTGCCTGAGAGCTGATCTGAGAGAC 2520
 Qy 2521 TGTGGCATCAGACCGAGTTGCCAGATCTGAGCTCAGCCCTGTGACAGACCGAGC 2580
 Db 2521 TGTGGCATCAGACCGAGTTGCCAGATCTGAGCTCAGCCCTGTGACAGACCGAGC 2580
 Qy 2581 TTGACACCTGTGTCTTCCACACAGCTGTGGGAAACGAGGTGTAATCTTACTGTGT 2640
 Db 2581 TTGACACCTGTGTCTTCCACACAGCTGTGGGAAACGAGGTGTAATCTTACTGTGT 2640
 Qy 2641 CGATCATGAGGCTTCCCACTGTAGTGTGAGAGGCTGATGATCAATGAGCCACCTG 2700
 Db 2641 CGATCATGAGGCTTCCCACTGTAGTGTGAGAGGCTGATGATCAATGAGCCACCTG 2700
 Qy 2701 GACACGCTGCTGTGTCTTCTGCACTTGGCTTATGAGTATCTCATGCTGACGAC 2760
 Db 2701 GACACGCTGCTGTGTCTTCTGCACTTGGCTTATGAGTATCTCATGCTGACGAC 2760
 Qy 2761 CTGAGCTTACATGAACTGTGAGAACATGAGCTGAGAGCTTCTGTGACAGGTATG 2820
 Db 2761 CTGAGCTTACATGAACTGTGAGAACATGAGCTGAGAGCTTCTGTGACAGGTATG 2820
 Qy 2821 AGAGAACATGCTGTGATCTCCAGAGCTGTGAGTGTGTAAGTGTCACTCAACGCGCG 2880
 Db 2821 AGAGAACATGCTGTGATCTCCAGAGCTGTGAGTGTGTAAGTGTCACTCAACGCGCG 2880
 Qy 2881 TGTGTGAGAGTGTCTGTGTGATCTGAGAGACAGACCTGAGAGCTGTGATCTG 2940
 Db 2881 TGTGTGAGAGTGTCTGTGTGATCTGAGAGACAGACCTGAGAGCTGTGATCTG 2940
 Qy 2941 ACGGACATGCTGTGAGAGCTGTGAGGCTGTGCTGTGAGAGGACCTGAGAGAG 3000
 Db 2941 ACGGACATGCTGTGAGAGCTGTGAGGCTGTGCTGTGAGAGGACCTGAGAGAG 3000
 Qy 3001 AACGATGCTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 3060
 Db 3001 AACGATGCTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 3060
 Qy 3061 GCACTCTCTGAGGCTTCTGCAACGAGCTGACCAAGTCTGAGGCTGTGAGGCT 3120
 Db 3061 GCACTCTCTGAGGCTTCTGCAACGAGCTGACCAAGTCTGAGGCTGTGAGGCT 3120

Db 3061 GCACTCTCTGAGGCTTCTGCAACGAGCTGACCAAGTCTGAGGCTGTGAGGCT 3120
 Qy 3121 AACCTCAGTCCCAAGAGATGAGAGCTGTGTGAGGCTTGTGCTGTCCAGCTTAA 3180
 Db 3121 AACCTCAGTCCCAAGAGATGAGAGCTGTGTGAGGCTTGTGCTGTCCAGCTTAA 3180
 Qy 3181 TTACAGATATGAGCTGTGAGAAATGAGAGCTGTGTGCAATGAGAGCTGTGAG 3240
 Db 3181 TTACAGATATGAGCTGTGAGAAATGAGAGCTGTGTGCAATGAGAGCTGTGAG 3240
 Qy 3241 GAGGTGAGCTTCTCAACCCGAGTCTTAAATGAGAGCTGTGTGCAATGAGAGCT 3300
 Db 3241 GAGGTGAGCTTCTCAACCCGAGTCTTAAATGAGAGCTGTGTGCAATGAGAGCT 3300
 Qy 3301 GATGACCAACAAATGAGACTTACTTCCGCTCCCTGAAAGCGGAGCTGAGCTAT 3360
 Db 3301 GATGACCAACAAATGAGACTTACTTCCGCTCCCTGAAAGCGGAGCTGAGCTAT 3360
 Qy 3361 GCTTGTGTGAGGAGTGAACCCAGAGAGAGAGAGCTGTGTGCTTCTGTGAGAG 3420
 Db 3361 GCTTGTGTGAGGAGTGAACCCAGAGAGAGAGAGCTGTGTGCTTCTGTGAGAG 3420
 Qy 3421 TTCAAGAGCTGACAGATTTGCCAGATCTCTGTGCTGAGCAAGCAATGTGATCC 3480
 Db 3421 TTCAAGAGCTGACAGATTTGCCAGATCTCTGTGCTGAGCAAGCAATGTGATCC 3480
 Qy 3481 CAGAGAGTGAACAAGTGAAGAGCTCCCGGCAACCATGAGAGAGAGAGAGAG 3540
 Db 3481 CAGAGAGTGAACAAGTGAAGAGCTCCCGGCAACCATGAGAGAGAGAGAGAG 3540
 Qy 3541 CAAGTAAATATGATGATGTGATATCCGAGCTGTGTGAACTGTGAGCTGAG 3600
 Db 3541 CAAGTAAATATGATGATGTGATATCCGAGCTGTGTGAACTGTGAGCTGAG 3600
 Qy 3601 GGGCTGTGATCAACAGTGTGATATCAACAGAGGATGAGCTGTGATCAACAG 3660
 Db 3601 GGGCTGTGATCAACAGTGTGATATCAACAGAGGATGAGCTGTGATCAACAG 3660
 Qy 3661 GAGCTGAGCTGAGGAGCTGTGTCCACAGTGTGATGAGCAACAGGAGTGTCTGT 3720
 Db 3661 GAGCTGAGCTGAGGAGCTGTGTCCACAGTGTGATGAGCAACAGGAGTGTCTGT 3720
 Qy 3721 CACTGAGAGCGGCTGTGAGGAGCTGTGTCTTAAAGTGTGATGAGCAACAG 3780
 Db 3721 CACTGAGAGCGGCTGTGAGGAGCTGTGTCTTAAAGTGTGATGAGCAACAG 3780
 Qy 3781 GTGTCTGTGATGAGAGGAGCTGTGAGGAGCTGTGTCTTAAAGTGTGATGAG 3840
 Db 3781 GTGTCTGTGATGAGAGGAGCTGTGAGGAGCTGTGTCTTAAAGTGTGATGAG 3840
 Qy 3841 CACAGCGTGTGAGCTGTGATCTGTGAGAGGCTGTGAGGCTGTGTCTTAAAGT 3900
 Db 3841 CACAGCGTGTGAGCTGTGATCTGTGAGAGGCTGTGAGGCTGTGTCTTAAAGT 3900
 Qy 3901 GGTATGAGCAACAGGAGTGTCTGTGATCTGTGAGAGGCTGTGAGGCTGTGTG 3960
 Db 3901 GGTATGAGCAACAGGAGTGTCTGTGATCTGTGAGAGGCTGTGAGGCTGTGTG 3960
 Qy 3961 TCCAAAGTGTGATGAGCAACAGGAGTGTCTGTGATCTGTGAGAGGCTGTGAG 4020
 Db 3961 TCCAAAGTGTGATGAGCAACAGGAGTGTCTGTGATCTGTGAGAGGCTGTGAG 4020
 Qy 4021 GGGCTGTGTCTTAA 4035
 Db 4021 GGGCTGTGTCTTAA 4035

RESULT 3
 US-10-860-761-3
 ; Sequence 3, Application US/10860761
 ; Publication No. US2004024875A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WYETH

QY 1798 TTCCAGACTCAAGACAAAGAGTTTGTGCTTGAGCAATTAACAGCTTCCAGAGAGTGTGG 1857
 Db 2074 TTCCAGACTCAAGACAAAGAGTTTGTGCTTGAGCAATTAACAGCTTCCAGAGAGTGTGG 2133
 QY 1858 CTTCCAGATTAAACAGAACCTTGACCTTGATAGCATTTCTTCTGCTCCAGACAGTGTCCG 1917
 Db 2134 CTTCCAGATTAAACAGAACCTTGACCTTGATAGCATTTCTTCTGCTCCAGACAGTGTCCG 2193
 QY 1918 TATTTGCGGAAAATTCGGGTGTGATGTCAAAAGGATCTTCCAGAGATGAGTCCCTGAG 1977
 Db 2194 TATTTGCGGAAAATTCGGGTGTGATGTCAAAAGGATCTTCCAGAGATGAGTCCCTGAG 2253
 QY 1978 GCATGCTCTGTGTGCTCTCTATGATGAGTGGGATTAAGACCTCATTTGAGGAGAGTGGGA 2037
 Db 2254 GCATGCTCTGTGTGCTCTCTATGATGAGTGGGATTAAGACCTCATTTGAGGAGAGTGGGA 2313
 QY 2038 GATTTCTGCTCCAGCTTGAGCAACCCACCACTGCGGAGCTGAGCTTGAGGAGCAGC 2097
 Db 2314 GATTTCTGCTCCAGCTTGAGCAACCCACCACTGCGGAGCTGAGCTTGAGGAGCAGC 2373
 QY 2098 ATCTTGAGAGAGCGGGCCATGAGAACCTGTGTGCAAGCTGAGGCAATCCCACTTGAG 2157
 Db 2374 ATCTTGAGAGAGCGGGCCATGAGAACCTGTGTGCAAGCTGAGGCAATCCCACTTGAG 2433
 QY 2158 ATACAGACCTTGATGTTAGAAATGACAGATTAACCTCTGTGTGAGAGACCTTGAGAG 2217
 Db 2434 ATACAGACCTTGATGTTAGAAATGACAGATTAACCTCTGTGTGAGAGACCTTGAGAG 2493
 QY 2218 ATGCTGATGACCAACCGTAACCTTAAGATCCCTCACTTGAGAGGAGCACTTGAGAG 2277
 Db 2494 ATGCTGATGACCAACCGTAACCTTAAGATCCCTCACTTGAGAGGAGCACTTGAGAG 2553
 QY 2278 GAGGATGTAAGATGAGCTGTGAGAACCTTAAGAACCCAAAATGTTTGTGAGAGCTTTG 2337
 Db 2554 GAGGATGTAAGATGAGCTGTGAGAACCTTAAGAACCCAAAATGTTTGTGAGAGCTTTG 2613
 QY 2338 AGGCTGATGCTGTGATGAGATGACCATGCTGTGATGAGATCTCCCAATCTTTAG 2397
 Db 2614 AGGCTGATGCTGTGATGAGATGACCATGCTGTGATGAGATCTCCCAATCTTTAG 2673
 QY 2398 ACCTCCCGCAGCCTGAAATCTTGAAGCTGTGAGAGAAACAAGTGAAGACAGAGAGTA 2457
 Db 2674 ACCTCCCGCAGCCTGAAATCTTGAAGCTGTGAGAGAAACAAGTGAAGACAGAGAGTA 2733
 QY 2458 ATGCTCTCAATGATGCTGTGAGATCTCCAGTGTGAGGCTGTGAGAGCTGATCTGAG 2517
 Db 2734 ATGCTCTCAATGATGCTGTGAGATCTCCAGTGTGAGGCTGTGAGAGCTGATCTGAG 2793
 QY 2518 GACTGTGATCAACAGCAGCGGTTGCAAGATGCTGAGCTGAGCTGTGAGAGCAACGG 2577
 Db 2794 GACTGTGATCAACAGCAGCGGTTGCAAGATGCTGAGCTGAGCTGTGAGAGCAACGG 2853
 QY 2578 AGCTTGACACACTGTGCTTAACCAACAAGCTGTGAGGAAACAAGTGTAAATCTACTG 2637
 Db 2854 AGCTTGACACACTGTGCTTAACCAACAAGCTGTGAGGAAACAAGTGTAAATCTACTG 2913
 QY 2638 TGTGATTCATGAGGCTTCCCACTGATGCTGAGAGGCTGATGCTGATGCTGAG 2697
 Db 2914 TGTGATTCATGAGGCTTCCCACTGATGCTGAGAGGCTGATGCTGATGCTGAG 2973
 QY 2698 CTGAGACAGGCTGTGCTGTGCTTCTGCACTGTGCTTAAAGGTAATCAATGCTGAG 2757
 Db 2974 CTGAGACAGGCTGTGCTGTGCTTCTGCACTGTGCTTAAAGGTAATCAATGCTGAG 3033
 QY 2758 CACCTGAGCTTGAAGATGAACCTGTGTGAGAGCAATGAGCTGAGAGCTTCTGTGAGAG 2817
 Db 3034 CACCTGAGCTTGAAGATGAACCTGTGTGAGAGCAATGAGCTGAGAGCTTCTGTGAGAG 3093
 QY 2818 ATGAGAGAACCAATCTTGTATCTCAAGACCTGAGGTTGTAAAGTGTATCTACCGCC 2877
 Db 3094 ATGAGAGAACCAATCTTGTATCTCAAGACCTGAGGTTGTAAAGTGTATCTACCGCC 3153

QY 2878 GCGTCTGTGAGAGTCTGTCTGTGTGATCTTGAGAGACAGACACTGTAAGAGCTTGAT 2937
 Db 3154 GCGTCTGTGAGAGTCTGTCTGTGTGATCTTGAGAGAGACAGACTGTAAGAGCTTGAT 3213
 QY 2938 CTCACGACCAATGCTTGTGTGAGAGCTGTGTGTGCTGTGTGTGCTGTGTGTGAGCA 2997
 Db 3214 CTCACGACCAATGCTTGTGTGAGAGCTGTGTGTGCTGTGTGTGCTGTGTGTGAGCA 3273
 QY 2998 AAGAACAGTGTCTGACAGAGCTGTGTGTGAGAGCATGTGAGCTGATGCTGTGTGT 3057
 Db 3274 AAGAACAGTGTCTGACAGAGCTGTGTGTGAGAGCATGTGAGCTGATGCTGTGTGT 3333
 QY 3058 GAGGCACTCTCTGT 3117
 Db 3334 GAGGCACTCTCTGT 3393
 QY 3118 AATTAATCTGATCCCAAGAGATGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3177
 Db 3394 AATTAATCTGATCCCAAGAGATGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3453
 QY 3178 AACTTAAGATTAATGT 3237
 Db 3454 AACTTAAGATTAATGT 3513
 QY 3238 GAGGAGTGTGAGCTTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3297
 Db 3514 GAGGAGTGTGAGCTTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3573
 QY 3298 GAGGATGACCGAGCAGC 3312
 Db 3574 GAGGATGACCGAGCAGC 3588

RESULT 4
 US-10-399-443-23
 ; Sequence 23, Application US/10399443
 ; Publication No. US200402869A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America, as Represented by the
 ; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
 ; APPLICANT: Health
 ; APPLICANT: Nelson, Lawrence M.
 ; APPLICANT: Tong, Zhi-Bin
 ; APPLICANT: Nelson, Lawrence
 ; APPLICANT: Zhi-Bin, Tong
 ; TITLE OF INVENTION: Human Gene Critical to Fertility
 ; FILE REFERENCE: 4239-64785
 ; CURRENT FILING DATE: 2003-04-16
 ; PRIOR FILING DATE: 2000-10-18
 ; PRIOR APPLICATION NUMBER: 60/241,510
 ; PRIOR APPLICATION NUMBER: PCT/US01/10981
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 3900
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3600)
 ; OTHER INFORMATION:
 ; US-10-399-443-23

Query Match 78.5%; Score 3166.2; DB 17; Length 3900;
 Best Local Similarity 96.2%; Pred. No. 0;
 Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

QY 1 ATGAGAGAGACCAATGCTCACTTTTCCAGCTACGGGCTGCAATGCTGTCTATGAG 60
 Db 154 ATGAGAGAGACCAATGCTCACTTTTCCAGCTACGGGCTGCAATGCTGTCTATGAG 213

QY 61 CTGACAGAGAAATTTCAACATTCAGAGAAATTAATAAGAGAAATCTTCAGATCG 120
Db 214 CTAGCAAGAGAAATTTCAACATTCAGAGAAATTAATAAGAGAAATCTTCAGAAATCG 273
QY 121 ACCACATGCTATTTCCACAGTTTGAATTCAGAAATGCGCAACGTGCAATGCTGCACTC 180
Db 274 ACCACATGCTATTTCCACAGTTTGAATTCAGAAATGCGCAACGTGCAATGCTGCACTC 333
QY 181 CTCTTCAGATGATTTATGAGCATCGTGGCTTGAGGCTAAGTCCATTTAGCATTTTGA 240
Db 334 CTCTTCAGATGATTTATGAGCATCGTGGCTTGAGGCTAAGTCCATTTAGCATTTTGA 393
QY 241 AACATGAACCTGCGAACCTCTCGAGAGAGCAAGGATGACATGAAAA----- 289
Db 394 AACATGAACCTGCGAACCTCTCGAGAGAGCAAGGATGACATGAAAAGACATTCACCA 453
QY 290 ----- 289
Db 454 GAAATCTCTGAAGCAACATGACTGACCAAGAGCAAGCAAGAGAAAAAGTCCAGGAATT 513
QY 290 -----AATTTCA 297
Db 514 TCACAGCTGTGCAACAGATAGTGCACAGCTGACAGACAAAAGAACAGAAATTTCA 573
QY 298 CAAGCTATGAAACAAAGAGTGCACAGACAGACAGACAAAGAAATTTCAACA 357
Db 574 CAAGCTATGAAACAAAGAGTGCACAGACAGACAGACAAAGAAATTTCAACA 633
QY 358 GCTATGAAACAAAGAGTGCACAGACAGACAGACAAAGAAATTTCAAGAGTAC 417
Db 634 GCTATGAAACAAAGAGTGCACAGACAGACAGACAAAGAAATTTCAAGAGTAC 693
QY 418 ACATGGAATCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGATGATAGTGT 477
Db 694 ACATGGAATCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGATGATAGTGT 753
QY 478 AGTTTGAACACATGCTGTGACTGAGCTGCAGAAATGCAACGTTGCTGTGAT 537
Db 754 AGTTTGAACACATGCTGTGACTGAGCTGCAGAAATGCAACGTTGCTGTGAT 813
QY 538 TCAGACCGTGGGGCTTCGAGCTGCGACAGTGTTCGACAGAAATTCAGAAATTTGGG 597
Db 814 TCAGACCGTGGGGCTTCGAGCTGCGACAGTGTTCGACAGAAATTCAGAAATTTGGG 873
QY 598 AAATGAGCTTACAGAGAGATCGTGTGCTGAGGCGCAAGTGAATCTTACCAAGGA 657
Db 874 AAATGAGCTTACAGAGAGATCGTGTGCTGAGGCGCAAGTGAATCTTACCAAGGA 933
QY 658 ATGTTCTCTACGTTCTTCTCCCTCCGTTAGAGATGACAGCGAGAGAGAGAGAGT 717
Db 934 ATGTTCTCTACGTTCTTCTCCCTCCGTTAGAGATGACAGCGAGAGAGAGAGAGT 993
QY 718 GTCACAGATTCATTCAGAGAGTGCACATCCAGGCTCCGAGTACAGAGATTCATG 777
Db 994 GTCACAGATTCATTCAGAGAGTGCACATCCAGGCTCCGAGTACAGAGATTCATG 1053
QY 778 TCCGACCAAGAAAGCTGTGTTTCATCATTCGATTCGATGACCTGAGGCTGTCTC 837
Db 1054 TCCGACCAAGAAAGCTGTGTTTCATCATTCGATTCGATGACCTGAGGCTGTCTC 1113
QY 838 AACCAATGACAAAGCTTCGCAAGACTGGGCTGAGAGAGAGCTCCGTTACCTCTATA 897
Db 1114 AACCAATGACAAAGCTTCGCAAGACTGGGCTGAGAGAGAGCTCCGTTACCTCTATA 1173
QY 898 CGCAGTCTGCTGAGAGAGTCTGCTCCCTGAGTCTTCTGATGTGACCTGACAGAC 957
Db 1174 CGCAGTCTGCTGAGAGAGTCTGCTCCCTGAGTCTTCTGATGTGACCTGACAGAC 1233
QY 958 GTGGGACAGAGAGCTCAAGTCAAGGTCGATCTCCCGTTACCTGTTAGTTAGAGA 1017
Db 1234 GTGGGACAGAGAGCTCAAGTCAAGGTCGATCTCCCGTTACCTGTTAGTTAGAGA 1293
QY 1018 ATCTCCGGGAAACAAAGATCCACTTGTCTCTTACGCGGGAATGCTGACATCCAGAG 1077

Db 1294 ATCTCCGGGAAACAAAGATCCACTTGTCTCTTACGCGGGAATGCTGACATCCAGAG 1353
QY 1078 ACACAGAGTTCGCTGCATCATGAACACCGTAGGCTGCTGACCAAGTGCAGGTGCGC 1137
Db 1354 ACACAGAGTTCGCTGCATCATGAACACCGTAGGCTGCTGACCAAGTGCAGGTGCGC 1413
QY 1138 GCGGTGGGCTCTCATCTGCGTGGCCCTGACGCTGACAGACGTGTGGGGAGAGCGTC 1197
Db 1414 GCGGTGGGCTCTCATCTGCGTGGCCCTGACGCTGACAGACGTGTGGGGAGAGCGTC 1473
QY 1198 GCCCCTTCAACCAAGCTTCAAGGCTGACAGCCCGCTTTGTTGTTTCACTCAAC 1257
Db 1474 GCCCCTTCAACCAAGCTTCAAGGCTGACAGCCCGCTTTGTTGTTTCACTCAAC 1533
QY 1258 CCTGAGGCGTGTGCGGCGCTGCTCAATCTGAGAGAGAAAGTGTCTGAAACGCTTC 1317
Db 1534 CCTGAGGCGTGTGCGGCGCTGCTCAATCTGAGAGAGAAAGTGTCTGAAACGCTTC 1593
QY 1318 TGCCGTATGCTGTGAGAGAGTGTGAATAGAAATCAAGTTCAGTGTGAGGACCTC 1377
Db 1594 TGCCGTATGCTGTGAGAGAGTGTGAATAGAAATCAAGTTCAGTGTGAGGACCTC 1653
QY 1378 ATGTTCAAGACCTCGGAGAGTGTGAGTCCGTGCTGTTTCAATGAACATCTTCTC 1437
Db 1654 ATGTTCAAGACCTCGGAGAGTGTGAGTCCGTGCTGTTTCAATGAACATCTTCTC 1713
QY 1438 CCAGACAGCCACTGTGAGAGTACTACACCTTCTTCAACCTCACTCCAGACCTTCTGT 1497
Db 1714 CCAGACAGCCACTGTGAGAGTACTACACCTTCTTCAACCTCACTCCAGACCTTCTGT 1773
QY 1498 GCGGCTTGTATCTACGTTTATAGAGGCGCTGAAATTCAGACCAAGCTCTGCGCTGTGAC 1557
Db 1774 GCGGCTTGTATCTACGTTTATAGAGGCGCTGAAATTCAGACCAAGCTCTGCGCTGTGAC 1833
QY 1558 GTTGAAGAGACAAAGAGTCCATGAGCTTAAACAGGCAAGCTTCCATATCACTCGCTT 1617
Db 1834 GTTGAAGAGACAAAGAGTCCATGAGCTTAAACAGGCAAGCTTCCATATCACTCGCTT 1893
QY 1618 TGGATGAAGCGTTCTTGTGTTGCGCTGATGAGCAAGCGTAAAGAGGCCACTGAGGTC 1677
Db 1894 TGGATGAAGCGTTCTTGTGTTGCGCTGATGAGCAAGCGTAAAGAGGCCACTGAGGTC 1953
QY 1678 CTGCTGGGCTGTCCGTTCCCTTGAGGAGTGAAGCAAGCTTCTGACTGGGTCTCTG 1737
Db 1954 CTGCTGGGCTGTCCGTTCCCTTGAGGAGTGAAGCAAGCTTCTGACTGGGTCTCTG 2013
QY 1738 TTGGGTGAGCAGGCTTAATGCGACACACCCAGAGACACCTGAGACGCTTCCACTGTCTT 1797
Db 2014 TTGGGTGAGCAGGCTTAATGCGACACACCCAGAGACACCTGAGACGCTTCCACTGTCTT 2073
QY 1798 TTGAGACTCAAGCAAAAGATTGTTGCTTGGCAATTAACAGCTTCAAGAGTGTG 1857
Db 2074 TTGAGACTCAAGCAAAAGATTGTTGCTTGGCAATTAACAGCTTCAAGAGTGTG 2133
QY 1858 CTTCCGATTAACAGAACTTGAATGACATCTTCTTCTGCTCCAGACTGTCCG 1917
Db 2134 CTTCCGATTAACAGAACTTGAATGACATCTTCTTCTGCTCCAGACTGTCCG 2193
QY 1918 TATTTGGGAAAAATTCGGGTGATGTCAAGAGATCTTCCAGAGATGAGTCCGCTGAG 1977
Db 2194 TATTTGGGAAAAATTCGGGTGATGTCAAGAGATCTTCCAGAGATGAGTCCGCTGAG 2253
QY 1978 GCATGCTGTGTCCTCTATGATGCGGGATTAAGACCTCATTTGAGAGCAATGGGAA 2037
Db 2254 GCATGCTGTGTCCTCTATGATGCGGGATTAAGACCTCATTTGAGAGCAATGGGAA 2313
QY 2038 GATTTCTGCTCATGCTTGGACCCACCACTCTGCGGAGCTGAGCTTGGAGCAGC 2097
Db 2314 GATTTCTGCTCATGCTTGGACCCACCACTCTGCGGAGCTGAGCTTGGAGCAGC 2373
QY 2098 ATCTGACAGAGCGGCGATGAGACCTGTGTCCAGCTGAGGCAATCCACTGCAAG 2157

Db 2314 ATCTGACAGAGCGGCGCATGAAAGCCTGTGTGCCAAGCTGAGGCACTCCAGCTGCAAG 2433
Qy 2158 ATACAGACCCCTGATTTTGAAGAATGACAGATTACCCCTGTGTGACAGACCTCTGAGAA 2217
Db 2454 ATACAGACCCCTGATTTTGAAGAATGACAGATTACCCCTGTGTGACAGACCTCTGAGAA 2493
Qy 2218 ATCTGATGAGCCAGCCTGTAACCTTAAGTCCCTCAACTTGGAGGACCCACTGAGAA 2277
Db 2494 ATCTGATGAGCCAGCCTGTAACCTTAAGTCCCTCAACTTGGAGGACCCACTGAGAA 2553
Qy 2278 GAGATGTGAAGATGCGCTGTGAAGCCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2337
Db 2554 GAGATGTGAAGATGCGCTGTGAAGCCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2613
Qy 2338 AGGCTGATGCTGTGATGATGACCTGATGCTGTGATGCTGATGCTGATGCTGATGCT 2397
Db 2614 AGGCTGATGCTGTGATGATGACCTGATGCTGTGATGCTGATGCTGATGCTGATGCT 2673
Qy 2398 AACTCCCGCAGCCTGATGCTGTGAGCCTGAGGAAACAGAGTGAACAGACCGAGAGTA 2457
Db 2674 AACTCCCGCAGCCTGATGCTGTGAGCCTGAGGAAACAGAGTGAACAGACCGAGAGTA 2733
Qy 2458 ATGCTCTGATGATGCTGATGAGTCTTCCAGTGTGCTGAGAGCTGAGATGATGAG 2517
Db 2734 ACGCTCTGATGATGCTGATGAGTCTTCCAGTGTGCTGAGAGCTGAGATGATGAG 2793
Qy 2518 GACTGTGATGATGAGCAGCAGGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2577
Db 2794 GACTGTGATGATGAGCAGCAGGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 2853
Qy 2578 AGCTTGACACACCTGTGCTATCCAAACAGCCTGAGGAAAGAGTGTGATGATGATG 2637
Db 2854 AGCTTGACACACCTGTGCTATCCAAACAGCCTGAGGAAAGAGTGTGATGATGATG 2913
Qy 2638 TGTGATGATGAGGCTTCCCACTGATGCTGAGAGCTGATGCTGATGCTGATGCTGAT 2697
Db 2914 TGTGATGATGAGGCTTCCCACTGATGCTGAGAGCTGATGCTGATGCTGATGCTGAT 2973
Qy 2698 CTGACAGGCTGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2757
Db 2974 CTGACAGGCTGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 3033
Qy 2758 CACCTGACCTTATGATGACCTGATGAGACCAATGAGGATGATGCTGATGAGTCTG 2817
Db 3034 CACCTGACCTTATGATGACCTGATGAGACCAATGAGGATGATGCTGATGAGTCTG 3093
Qy 2818 ATGAGAGAACCACTTGTGATGCTGAGACCTGAGAGTGTGATGATGATGATGATG 2877
Db 3094 ATGAGAGAACCACTTGTGATGCTGAGACCTGAGAGTGTGATGATGATGATGATG 3153
Qy 2878 GCGTCTGTGAGAGTGTGCTGTGTGTGATCTGAGAGACCACTGATGAGTCTGATG 2937
Db 3154 GCGTCTGTGAGAGTGTGCTGTGTGTGATCTGAGAGACCACTGATGAGTCTGATG 3213
Qy 2938 CTGACGACCAATGCTGAGGATGAGGAGTGTGCTGAGGATGAGGAGTGTGAGGAGT 2997
Db 3214 CTGACGACCAATGCTGAGGATGAGGAGTGTGCTGAGGATGAGGAGTGTGAGGAGT 3273
Qy 2998 AAGAACAGTGTGCTGACAGACCTGAGTGTGAGAGCAGTGTGATGATGATGATG 3057
Db 3274 AAGAACAGTGTGCTGACAGACCTGAGTGTGAGAGCAGTGTGATGATGATGATG 3333
Qy 3058 GAGGACCTGTGCTGAGGCTTCTGAGACCGGATGAGACAGTGTGATGATGATGATG 3117
Db 3334 GAGGACCTGTGCTGAGGCTTCTGAGACCGGATGAGACAGTGTGATGATGATGATG 3393
Qy 3118 AATACTCAGTCCCAAGAGATGATGAGTGTGAGGCTTGTGCTGCTGCTGCTGCTGCT 3177
Db 3394 AATACTCAGTCCCAAGAGATGATGAGTGTGAGGCTTGTGCTGCTGCTGCTGCTGCT 3453
Qy 3178 AACTTACAGATGATGAGGCTGTGAGATGAGCAGTGTGATGATGATGATGATGATG 3237
Db 3454 AACTTACAGATGATGAGGCTGTGAGATGAGCAGTGTGATGATGATGATGATGATG 3513

Qy 3238 GAGGAGTGTGAGTGTGATGAGGCTGAGTGTGATGAGGCTGAGTGTGATGAGTGTGAT 3297
Db 3514 GAGGAGTGTGAGTGTGATGAGGCTGAGTGTGATGAGGCTGAGTGTGATGAGTGTGAT 3573
Qy 3298 GAGGAGTGTGAGTGTGATGAGGCTGAGTGTGATGAGGCTGAGTGTGATGAGTGTGAT 3312
Db 3574 GAGGAGTGTGAGTGTGATGAGGCTGAGTGTGATGAGGCTGAGTGTGATGAGTGTGAT 3588

RESULT 5
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (3600)
US-10-677-943-23

Query Match 78.5%; Score 316.2; DB 17; Length 3900;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

Qy 1 ATGAGAGAGACCAATGCTGATGCTTTCAGCTGAGGCTGAGTGTGATGATGATGATG 60
Db 154 ATGAGAGAGACCAATGCTGATGCTTTCAGCTGAGGCTGAGTGTGATGATGATGATG 213
Qy 61 CTAGACAGAGAAATTTTCAAGCAATTTCAAGAAATTTCAAGAAATTTTCAAGAAATTT 120
Db 214 CTAGACAGAGAAATTTTCAAGCAATTTCAAGAAATTTTCAAGAAATTTTCAAGAAATTT 273
Qy 121 ACCACATGCTTATTTCAAGATTTGAATGAGATGAGATGAGATGAGATGAGATGAGATG 180
Db 274 ACCACATGCTTATTTCAAGATTTGAATGAGATGAGATGAGATGAGATGAGATGAGATG 333
Qy 181 CTCTGATGAGATTTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 240
Db 334 CTCTGATGAGATTTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 393
Qy 241 AACATGAACTGCGAACCTCTCGGAGAGGACGAGGATGAGATGAGATGAGATGAGATG 289
Db 394 AACATGAACTGCGAACCTCTCGGAGAGGACGAGGATGAGATGAGATGAGATGAGATG 453
Qy 290 ----- 289
Db 454 GAGATCTGAGAGACAGATGATGAGACAGAGACAGAGAGAGAGAGAGAGAGAGATG 513
Qy 290 -----AATTCA 297
Db 514 TCACAGCTGTGACACAGATGATGACAGCTGAGAGACAGAGAGAGAGAGAGAGATTTCA 573

QY 298 CAAGCTATGGAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 357
 Db 574 CAAGCTATGGAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 633
 QY 358 GCTATGGAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 417
 Db 634 GCTATGGAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 693
 QY 418 ACATGGGACTACAGAGTCAAGTATGACAAATTCGCTGAGAGAGATGTAAGTCTGT 477
 Db 694 ACATGGGACTACAGAGTCAAGTATGACAAATTCGCTGAGAGAGATGTAAGTCTGT 753
 QY 478 AGTTTGAACAACCTGCTGCTGAGTGGCCGGAATGCAACGTTGGCTGTGTTGAT 537
 Db 754 AGTTTGAACAACCTGCTGCTGAGTGGCCGGAATGCAACGTTGGCTGTGTTGAT 813
 QY 538 TCAGACCGGTGGGGCTTCGGGCTTCGCAAGGTGTTGCAAGGAATGCAAGAAATGGG 597
 Db 814 TCAGACCGGTGGGGCTTCGGGCTTCGCAAGGTGTTGCAAGGAATGCAAGAAATGGG 873
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 Db 874 AAATCGGCTAGCCAGAGAGATCGTGTGCTGTGGCGCAAGGTGACTCTACCAAGGA 933
 QY 658 ATGTTCTCTAAGTCTTCTCTCCGCTTGAAGATGACAGCGAAGAGAGAGAGT 717
 Db 934 ATGTTCTCTAAGTCTTCTCTCCGCTTGAAGATGACAGCGAAGAGAGAGAGT 993
 QY 718 GTCAAGAGTTCATCTCCAGAGAGTGGCACAATCCAGGCTCCGGTGAACGAATCAATG 777
 Db 994 GTCAAGAGTTCATCTCCAGAGAGTGGCACAATCCAGGCTCCGGTGAACGAATCAATG 1053
 QY 778 TCCGACCAAGAAAGGCTGTGTCATCATGACGAGTTTCATGACCTGGGCTGTCTCTC 837
 Db 1054 TCCGACCAAGAAAGGCTGTGTCATCATGACGAGTTTCATGACCTGGGCTGTCTCTC 1113
 QY 838 AACATGACACAAAGCTCTGCAAGAGCTGGGCTGAGAGAGAGAGAGAGTCCCTCA 897
 Db 1114 AACATGACACAAAGCTCTGCAAGAGCTGGGCTGAGAGAGAGAGAGAGTCCCTCA 1173
 QY 898 CGCAGTCTGAGAGAGAGTCTGTCTCCGTAGTCCCTGATGCTGACAGTCAAGAGAC 957
 Db 1174 CGCAGTCTGAGAGAGAGTCTGTCTCCGTAGTCCCTGATGCTGACAGTCAAGAGAC 1233
 QY 958 GTGGGACACAGAGAGCTCAAGTCAAGAGTCTGTCTCCGTATCACTGTATGAGAGA 1017
 Db 1234 GTGGGACACAGAGAGCTCAAGTCAAGAGTCTGTCTCCGTATCACTGTATGAGAGA 1293
 QY 1018 ATCTCCGGGAAACAAGAAATCACTTGTCTTTGAGCGGGATTTGTGACATCAGAA 1077
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 Db 1354 ACACAAAGGTTGGTGGCATCATGAAACAACGTGAGTCTGACCAATGCGCAGTGGCC 1413
 QY 1138 GCCGTGGGCTCTCATCTGCGTGGCCCTGACGCTGACAGAGTGGTGGGGAGAGCGTC 1197
 Db 1414 GCCGTGGGCTCTCATCTGCGTGGCCCTGACGCTGACAGAGTGGTGGGGAGAGCGTC 1473
 QY 1198 GCCCCCTTCAACAACGCTCAACAGGCTGCAAGCGCGCTTTGTGTTTCATCACTCAC 1257
 Db 1474 GCCCCCTTCAACAACGCTCAACAGGCTGCAAGCGCGCTTTGTGTTTCATCACTCAC 1533
 QY 1258 CCTGAGAGCGTGGTCCGCGCTGTCTCATCTGAGAGAAAGATTGTCTTGAAGCGCTTC 1317
 Db 1534 CCTGAGAGCGTGGTCCGCGCTGTCTCATCTGAGAGAAAGATTGTCTTGAAGCGCTTC 1593
 QY 1318 TGCCGTATGCGCTGAGAGAGTGTGAATAGAAAGTCAAGTGTGATGAGTGAAGACCTC 1377
 Db 1594 TGCCGTATGCGCTGAGAGAGTGTGAATAGAAAGTCAAGTGTGATGAGTGAAGACCTC 1633
 QY 1378 ATGTTCAAGAGCTCGGAGAGTCTGAGCTCCGTGCTGTGTTCAATGAAACATCTTCTC 1437

Db 1454 ATGTTCAAGAGCTCGGAGAGTCTGAGCTCCGTGCTGTGTTCAATGAACATCTTCTC 1713
 QY 1438 CCAGACAGCCACTGTGAGAGTACTACACTTCTTCCACTCACTCACTCAAGACCTTCTGT 1497
 Db 1714 CCAGACAGCCACTGTGAGAGTACTACACTTCTTCCACTCACTCACTCAAGACCTTCTGT 1773
 QY 1498 GCCCCTTGTATCAAGTGTGAGAGGCGCTGGAATTCAGACCAAGCTCTCTGCTCTGTAC 1557
 Db 1774 GCCCCTTGTATCAAGTGTGAGAGGCGCTGGAATTCAGACCAAGCTCTCTGCTCTGTAC 1833
 QY 1558 GTTGAAGAACAAAGAGTCCATGAGAGCTTAAACAGCAGGCTTCCATATCCACTGCTT 1617
 Db 1834 GTTGAAGAACAAAGAGTCCATGAGAGCTTAAACAGCAGGCTTCCATATCCACTGCTT 1893
 QY 1618 TGATGAAGAGCTTCTTGTGAGCGCTGATGACGAACGTAAGAGAGCCACTGAAGTTC 1677
 Db 1894 TGATGAAGAGCTTCTTGTGAGCGCTGATGACGAACGTAAGAGAGCCACTGAAGTTC 1953
 QY 1678 CTGCTGGGCTGTCCCGTTCCCTGGGGGTGAAGCAGAAAGCTTGTGACTGAGTCTCTG 1737
 Db 1954 CTGCTGGGCTGTCCCGTTCCCTGGGGGTGAAGCAGAAAGCTTGTGACTGAGTCTCTG 2013
 QY 1738 TTGGGTCAAGAGCTTAATGCAACCAAGCAGAGAGACCTGTGAGCGCTTCCACTGTCTT 1797
 Db 2014 TTGGGTCAAGAGCTTAATGCAACCAAGCAGAGAGACCTGTGAGCGCTTCCACTGTCTT 2073
 QY 1798 TTGAGACTCAAGACAAAGATTGTTGAGCTGGCAATTAACAGCTTCCAAGAGTGTG 1857
 Db 2074 TTGAGACTCAAGACAAAGATTGTTGAGCTGGCAATTAACAGCTTCCAAGAGTGTG 2133
 QY 1858 CTTCCAGATTAACAGAACTGAGACTTATGACATCTTCTGTGCTCAAGACTGTCTCG 1917
 Db 2134 CTTCCAGATTAACAGAACTGAGACTTATGACATCTTCTGTGCTCAAGACTGTCTCG 2193
 QY 1918 TATTTGGGAAAAATTCGGGTGAGATGTCAAGAGATCTTCCCAAGATGAGTCCGCTGAG 1977
 Db 2194 TATTTGGGAAAAATTCGGGTGAGATGTCAAGAGATCTTCCCAAGATGAGTCCGCTGAG 2253
 QY 1978 GCATGCTCTGTGTCCTCTATGAGATCGGGATTAAGACCTCATTTGAGAGACATGGGAA 2037
 Db 2254 GCATGCTCTGTGTCCTCTATGAGATCGGGATTAAGACCTCATTTGAGAGACATGGGAA 2133
 QY 2038 GATTTCTGCTCATGCTTGGGACCCACCAACCACTGTGGGAGCTGACCTTGGGAGCAG 2097
 Db 2214 GATTTCTGCTCATGCTTGGGACCCACCAACCACTGTGGGAGCTGACCTTGGGAGCAG 2373
 QY 2098 ATCTGACAGAGCGGGCCATGAGAGACCTGTGTGCCAAGCTGAGGCAATCCACTGCAAG 2157
 Db 2274 ATCTGACAGAGCGGGCCATGAGAGACCTGTGTGCCAAGCTGAGGCAATCCACTGCAAG 2433
 QY 2158 ATACAGACCCGTGATTTAAGAAATGCAAGATTACCCCTGGTGTGACAGACCTTGGAGA 2217
 Db 2434 ATACAGACCCGTGATTTAAGAAATGCAAGATTACCCCTGGTGTGACAGACCTTGGAGA 2493
 QY 2218 ATGCTATGAGCAACCGTTAACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAAGAA 2277
 Db 2494 ATGCTATGAGCAACCGTTAACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAAGAA 2553
 QY 2278 GAGATGTAAGATGCGGTGTGAAGCTTAAACCAACCAAAATTTGTTGAGAGTCTTTG 2337
 Db 2554 GAGATGTAAGATGCGGTGTGAAGCTTAAACCAACCAAAATTTGTTGAGAGTCTTTG 2613
 QY 2238 AGGCTGAATGCTGTGATTTGAACCAATGCGCTTAACTGAAGATCTCCAAATCTTACG 2397
 Db 2614 AGGCTGAATGCTGTGATTTGAACCAATGCGCTTAACTGAAGATCTCCAAATCTTACG 2673
 QY 2398 ACTTCCCGCAGCCTGAATCTCTGAGCCTGGCAGAGAAACAAGTGAAGACCAAGAGTA 2457
 Db 2674 ACTTCCCGCAGCCTGAATCTCTGAGCCTGGCAGAGAAACAAGTGAAGACCAAGAGTA 2733
 QY 2458 ATGCTTCAAGTATGCTTGAAGAGTCTCCAGTGGCGCCTGCAAGAGCTGATCTGAGAG 2517

Db 2734 ACGCCTCTAGTATGCTTGAAGGCTCTCCAGATGCGCCCTGACAGAACTGATCTGAG 2793
QY GACTGTGATCAGACGCGGTTTGCAAGTCTGAGCTGAGCCCTGACGAAACGG 2577
Db 2794 GACTGTGATCAGACGCGGTTTGCAAGTCTGAGCTGAGCCCTGACGAAACGG 2853
QY AGCTTGACACACTGTGCTTATCCAAACAAGCCCTGGGAAAGAGTGAATCTACTG 2637
Db 2638 AGCTTGACACACTGTGCTTATCCAAACAAGCCCTGGGAAAGAGTGAATCTACTG 2913
QY TGTGATTCATGAGGCTTCCCACTGATGCTGACAGAGCTGATCTGAATCAGTCCAC 2697
Db 2698 TGTGATTCATGAGGCTTCCCACTGATGCTGACAGAGCTGATCTGAATCAGTCCAC 2973
QY CTGACACGCGCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 2757
Db 2758 CTGACACGCGCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 3033
QY CACCTGAGCTTATGATGAAACCTGTGAGAAACAATGCGTGAAGCTTCTGTGCGAGGTC 2817
Db 3034 CACCTGAGCTTATGATGAAACCTGTGAGAAACAATGCGTGAAGCTTCTGTGCGAGGTC 3093
QY ATGAGAGAACCATCTTGTCTATCTCCAGGACCTGAGGTTGTTAAGTCTCATCTCACGCC 2877
Db 3094 ATGAGAGAACCATCTTGTCTATCTCCAGGACCTGAGGTTGTTAAGTCTCATCTCACGCC 3153
QY GCGTCTGTGAGAGTCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 2937
Db 2938 GCGTCTGTGAGAGTCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 3213
QY CTACGAGCAATGCTGCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 2997
Db 3214 CTACGAGCAATGCTGCTGCTGCTGCTTCTTCACTGCGCTTATGAGGTAATCATGCTGACG 3273
QY AAGAAAGTCTTCTGACGAGACTGCGGTTGAAAGGATGAGCTGATCTGATTTGCTGT 3057
Db 3058 AAGAAAGTCTTCTGACGAGACTGCGGTTGAAAGGATGAGCTGATCTGATTTGCTGT 3333
QY GAGGCACTCTCTGAGGCTTCTTCTGCAACCGGCACTGACGAGCTGATCTGATTTGCTGT 3117
Db 3334 GAGGCACTCTCTGAGGCTTCTTCTGCAACCGGCACTGACGAGCTGATCTGATTTGCTGT 3393
QY AATACTTCAGTCCCAAGAAATGATGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3177
Db 3394 AATACTTCAGTCCCAAGAAATGATGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3453
QY AACTTACAGATTAATTTGGGCTGTGAAATGGCAGTACCTGTGCAAAATAGGAAGCTGCTG 3237
Db 3454 AACTTACAGATTAATTTGGGCTGTGAAATGGCAGTACCTGTGCAAAATAGGAAGCTGCTG 3513
QY GAGGAGTGCAGCTTCTGAGGCTTCTGCAACCGGCACTGACGAGCTGATCTGATTTGCTGT 3297
Db 3514 GAGGAGTGCAGCTTCTGAGGCTTCTGCAACCGGCACTGACGAGCTGATCTGATTTGCTGT 3573
QY GAGAGTGCAGCAGAC 3312
Db 3574 GAGAGTGCAGCAGTAC 3588

RESULT 6
US-10-216-645-3

Sequence 3, Application US/10216645
Publication No. US20030125282A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
APPLICANT: LESSL, MONIKA
APPLICANT: PETERS-KOTTIG, MICHAEL
APPLICANT: BECKMANN, GEORG
TITLE OF INVENTION: HUMAN WATER PROTEINS
FILE REFERENCE: SCH-1910
CURRENT APPLICATION NUMBER: US/10/216,645
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 101 39 874.3 41

PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3830
TYPE: DNA
ORGANISM: Homo sapiens
US-10-216-645-3

Query Match 77.8%; Score 3139; DB 15; Length 3830;
Best Local Similarity 96.0%; Fred. No. 0;
Matches 3282; Conservative 0; Mismatches 30; Indels 105; Gaps 2;

QY 1 ATGAGAGAGCAATATGCTGACCTTTCCAGCTACGCGGCTGCAATGCTGCTATAG 60
Db 1 ATGAGAGAGCAATATGCTGACCTTTCCAGCTACGCGGCTGCAATGCTGCTATAG 60
QY 61 CTAGCAAGAGAAATTTCAACATTCAGAAATTTACTAAAGAAATTTCTAGAAATCG 120
Db 61 CTAGCAAGAGAAATTTCAACATTCAGAAATTTACTAAAGAAATTTCTAGAAATCG 120
QY 121 ACCAATGCTTATTTCCAGATTTGAATTCAGAAATGCAACGCGGAAATGCTGCAATC 180
Db 121 ACCAATGCTTATTTCCAGATTTGAATTCAGAAATGCAACGCGGAAATGCTGCAATC 180
QY 181 CTCTTGATGATGATTTATGAGCATGCTGCGCTGCGGCTGCAATGCTGCTGCTGCTG 240
Db 181 CTCTTGATGATGATTTATGAGCATGCTGCGCTGCGGCTGCAATGCTGCTGCTGCTG 240
QY 241 AACATGAACTGCGAACCCTCTCGGAGAGGCAAGGATGACATGAAAAATTTACAA 300
Db 241 AACATGAACTGCGAACCCTCTCGGAGAGGCAAGGATGACATGAAAAATTTACAA 300
QY 301 GCT-----ATGAAACAGAGAGTCCACAGACAGAGACAGAAACA- 344
Db 301 GATCTGAGCAAGATGACATGACCAAGACCAAGCAAGAAATGTCAGAAATTA 360
QY 345 ----- 344
Db 361 TATGCAATGACTAAGCTTATCTTGGGGGTGCTGACATCTGACTCGAATTAACAC 420
QY 345 -----AGAAATTTCAAGCTATGAAACAGAGGT 375
Db 421 AAGTATGTTGAATTCATTTCTTTTTCAGAAATTTCAAGGATGAGAAAGGT 480
QY 376 GCCACAGCAGAGACAGAGAAACAAGACATGAGGTGACATGAGGACTACAGAGT 435
Db 481 GCCACAGCAGAGACAGAGAAACAAGACATGAGGTGACATGAGGACTACAGAGT 540
QY 436 CAGGTGAGACCAATTCGCTGAGAGAGAGATGTAAGTCTGTTGAAACATGCT 495
Db 541 CAGGTGAGACCAATTCGCTGAGAGAGAGATGTAAGTCTGTTGAAACATGCT 600
QY 496 GCTGATGCGCGGAAATGCAAACTTGGCTGCTGCTTTTGAATGACCGGTGCGGCTTC 555
Db 601 GCTGATGCGCGGAAATGCAAACTTGGCTGCTGCTTTTGAATGACCGGTGCGGCTTC 660
QY 556 CGGCTCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Db 661 CGGCTCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 616 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Db 721 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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Db 781 TTCTCCCGCTTGAAGATGACAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 736 AGGAGTGGCCAGACTCCAGGCTCCGCTGACGAGATCATGCTCCGACAGAAAGCTG 795
Db 841 AGGAGTGGCCAGACTCCAGGCTCCGCTGACGAGATCATGCTCCGACAGAAAGCTG 900

Qy 796 TTGTTCAATTCAGACGGTTTGGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 855
Db 901 TTGTTCAATTCAGACGGTTTGGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 960
Qy 856 TGCAGAGCTGGGGCTGAGAGCAGCTCCGTTCAACCCATACCGAGCTGCTGAGAG 915
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RESULT 8

US-10-216-645-1

; Sequence 1, Application US/10216645

; Publication No. US20030125282A1

; GENERAL INFORMATION:

; APPLICANT: WEISS, BERTRAM

; APPLICANT: LESSL, MONIKA


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1  APPLICANT: PETERS-KOTTIG, MICHAEL
2  APPLICANT: BECKMANN, GEORG
3  TITLE OF INVENTION: HUMAN MATER PROTEINS
4  FILE REFERENCE: SCH-1910
5  CURRENT APPLICATION NUMBER: US/10/216,645
6  CURRENT FILING DATE: 2003-01-21
7  PRIOR APPLICATION NUMBER: DE 101 39 874.3 411
8  PRIOR FILING DATE: 2001-08-10
9  NUMBER OF SEQ ID NOS: 11
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO 1
12     LENGTH: 3926
13     TYPE: DNA
14 ORGANISM: Homo sapiens
15 US-10-216-645-1

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Query Match	77.7%	Score 3133.6	DB 15	Length 3926
Best Local Similarity	95.2%	Pred No. 0		
Matches 3308	Conservative 0	Mismatches 4	Indels 162	Gaps 1

QY	1	ATGGAAGAGACAATAATCGCTCACTTTTCACGTACGAGGCTGGAATGAGTCTATAGAG	60
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Db	61	CTAGACAAGAGAATTTTCAGACATTCAGAGATTACTAAGAGAAATCTTCAGATCG	120
QY	121	ACCAATGCTCTATTCACAGTTTGAATTCGAAATCGCAAGTGTCTGGCACTC	180
Db	121	ACCAATGCTCTATTCACAGTTTGAATTCGAAATCGCAAGTGTCTGGCACTC	180
QY	181	CTCTTGACATGATATTTATGAGACATCGCTGGCTGACGTCCATTTAGCATCTTTGAA	240
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Db	241	AACATGAACCTGCGAACCTCTTCGGAGAAAGCACCAGATGACATGAAA-----	289
QY	290	-----	289
Db	301	GATCCTGAAGCAACGATGACTGACCCAGAGCAACAGAGAAAAGTCCAGAAAATAAA	360
QY	290	-----	289
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QY	290	-----AAATTTCAACAGCTATGGAACAAGAGT	318
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QY	379	ACAGCAGACAGACAGAGAAACAAGACAATGAGGTGACACATGAGGACTACAAGATCAC	438
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QY	439	GTCATGACCAATTCGCTGAGAGAGAGATGATCGTGTAGTTTGAACACATGCTGCT	498
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QY	499	GACATGCGCGGAAATCCGAAACGTTTGCTGGTGCCTTTGATTCAGACCGGTGGGGCTTCCGG	558
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Qy 2659 CACTGTAGTCTGAGAGGCTGATGCTGAATCATGTCACCTGGAACGCGCTGGCTGTGGT 2718
Db 2821 CACTGTAGTCTGAGAGGCTGATGCTGAATCATGTCACCTGGAACGCGCTGGCTGTGGT 2880
Qy 2719 TTTCTTGAATTGGCTTATGAGTAACTCATGCTGACGCACTGAGCTTATGATGAAC 2778
Db 2881 TTTCTTGAATTGGCTTATGAGTAACTCATGCTGACGCACTGAGCTTATGATGAAC 2940
Qy 2779 CTTGTGAAGACATGGGTGAAGCTTCTGTGCGAGGTGATGAGAGAACTTTGTTCAT 2838
Db 2941 CTTGTGAAGACATGGGTGAAGCTTCTGTGCGAGGTGATGAGAGAACTTTGTTCAT 3000

Qy 2839 CTCCAGGACCTGAGATTGTTAAATGTCATCTCAACGCGCGGTGCTGTGAGATCTGTCC 2898
Db 3001 CTCCAGGACCTGAGATTGTTAAATGTCATCTCAACGCGCGGTGCTGTGAGATCTGTCC 3060
Qy 2899 TGTGTATCTGAGAGACAGACACTGAAGAGCTGTGATCTCAACGCAATGCTGGGT 2958
Db 3061 TGTGTATCTGAGAGACAGACACTGAAGAGCTGTGATCTCAACGCAATGCTGGGT 3120
Qy 2959 GACGGTGGGTGTGTGCGCTGTGCGAGGACTGAAGCAAAAGAACAGTGTCTGACAGA 3018
Db 3121 GACGGTGGGTGTGTGCGCTGTGCGAGGACTGAAGCAAAAGAACAGTGTCTGACAGA 3180
Qy 3019 CTCGGTTGAAGGATGTGACTGACTTCTGATTTGCTGTGAGGCACTCTCTGGCCCTT 3078
Db 3181 CTCGGTTGAAGGATGTGACTGACTTCTGATTTGCTGTGAGGCACTCTCTGGCCCTT 3240
Qy 3079 TCCGCAACCGGCACTGACCAAGCTGATGAGATGATGAGTATGCTCAAGTCCCAAGGA 3138
Db 3241 TCCGCAACCGGCACTGACCAAGCTGATGAGATGATGAGTATGCTCAAGTCCCAAGGA 3300
Qy 3139 ATGATGAAGCTGTGTGCGCTTGTGCTGCCAGCTCTAACTTACAGATTAATGGCTG 3198
Db 3301 ATGATGAAGCTGTGTGCGCTTGTGCTGCCAGCTCTAACTTACAGATTAATGGCTG 3360
Qy 3199 TGAATGAGCAATACCTGTGCAAAATGAAGAGCTGTGAGAGAGTCACTCAAG 3258
Db 3361 TGAATGAGCAATACCTGTGCAAAATGAAGAGCTGTGAGAGAGTCACTCAAG 3420
Qy 3259 CCCGAGTCTTAATGAACGATGTTGGCATCTTTTGAATGAATGACCAACG 3312
Db 3421 CCCGAGTCTTAATGAACGATGTTGGCATCTTTTGAATGAATGACCAACG 3474

RESULT 9
US-10-092-900A-347
Sequence 347, Application US/10092900A
Publication No. US2004004382A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ut, Weizhen
APPLICANT: Gorman, Linda
APPLICANT: Miller, Charles E.
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Gangoli, Beba A.M.
APPLICANT: Vermet, Corine A.M.
APPLICANT: Guo, Xiaojia Saeha
APPLICANT: Tchernev, Velizar T.
APPLICANT: Fernandes, Elma R.
APPLICANT: Caeman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Gerlach, Valerie
APPLICANT: Liu, Yi
APPLICANT: Anderson, David W.
APPLICANT: Spaderna, Steven K.
APPLICANT: Carterton, Elina
APPLICANT: Leite, Mario W.
APPLICANT: Zhong, Haihong
APPLICANT: Alsobrook, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine B.
TITLE OR INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-290C
CURRENT APPLICATION NUMBER: US/10/092,900A

CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/283,675
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: USN 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: USN 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/274,191
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/325,681
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: USN 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USN 60/279,995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USN 60/294,899
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: USN 60/287,424
PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
SEQ ID NO 347
LENGTH: 3226
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (69)..(3168)
US-10-092-900A-347

Query Match 71.9%; Score 2900.6; DB 17; Length 3226;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 406 CATGAGGTGACACATGAGGACCTACAGAGTACGATGACCAATTTGCTGAGGAGGAG 465
DB 249 CATGAGGTGACACATGAGGACCTACAGAGTACGATGACCAATTTGCTGAGGAGGAG 308
QY 466 GATGTAAGTCTGATGTTTGAAGAACATGCTGCTGCTGCGCGGAATGCAACGTTGCT 525
DB 309 GATGTAAGTCTGATGTTTGAAGAACATGCTGCTGCTGCGCGGAATGCAACGTTGCT 368
QY 526 GGTGCTTTTGAATCAAGACCGGTGGGCTTCCGGCTCCGACGGTGTCTGACGGAAG 585
DB 369 GGTGCTTTTGAATCAAGACCGGTGGGCTTCCGGCTCCGACGGTGTCTGACGGAAG 428
QY 586 TCAGGAATTGGGAATGGGCTCTAGCCAGAGGATCGTGTGCTGGGCGCAAGTGA 645
DB 429 TCAGGAATTGGGAATGGGCTCTAGCCAGAGGATCGTGTGCTGGGCGCAAGTGA 488
QY 646 CTCTACAGGAGGATGTTCTCTACGCTTCTTCCCTCCCGTTAGAGAGATCAAGCGGAG 705
DB 489 CTCTACAGGAGGATGTTCTCTACGCTTCTTCCCTCCCGTTAGAGAGATCAAGCGGAG 548
QY 706 AAGGAGAGCATGTCTACAGAGTTCCTCAGAGAGTGGCCAGACTCCCAAGCTCCGGTG 765
DB 549 AAGGAGAGCATGTCTACAGAGTTCCTCAGAGAGTGGCCAGACTCCCAAGCTCCGGTG 608
QY 766 ACGGAGATCATGTCCCGACAGAAAGCTGTGTTCATCATTTGACGTTGGATGAGACTG 825
DB 609 ACGGAGATCATGTCCCGACAGAAAGCTGTGTTCATCATTTGACGTTGGATGAGACTG 668
QY 826 GGTCTGTCTCTCAACATGACAAAGCTCTGCAAAAGCTGGCTGAGAGCAAGCTTCG 885
DB 669 GGTCTGTCTCTCAACATGACAAAGCTCTGCAAAAGCTGGCTGAGAGCAAGCTTCG 728
QY 886 TTCAACCTCATACGACATCTGCTGAGAAAGTCTGCTCCCTGAGTCTTCTGATCTC 945
DB 729 TTCAACCTCATACGACATCTGCTGAGAAAGTCTGCTCCCTGAGTCTTCTGATCTC 788
QY 946 ACGCTCAGAGACGTGGGACAGAGAGCTCAAGTCAAGAGTCTGCTCCCGTTACTG 1005

DB 789 ACCGTCAAGACGTGGGACAGAGAGCTCAAGTCAAGAGTCTGCTCCCGTTACTG 848
QY 1006 TTAGTTAAGAGATTCCTCGGGAAACAAGATTCACCTTGCTCTTGAACCGGGATTGT 1065
DB 849 TTAGTTAAGAGATTCCTCGGGAAACAAGATTCACCTTGCTCTTGAACCGGGATTGT 908
QY 1066 GAGCATCAGAGACACAGAGGTGGTGCATCATGAAACAACCGTGAAGCTGCTGACGAG 1125
DB 909 GAGCATCAGAGACACAGAGGTGGTGCATCATGAAACAACCGTGAAGCTGCTGACGAG 968
QY 1126 TGCCAGGTGCGCGCGTGGGCTTCTCATCTGCGTGGCTTCAGCTGACAGACGTGTG 1185
DB 969 TGCCAGGTGCGCGCGTGGGCTTCTCATCTGCGTGGCTTCAGCTGACAGACGTGTG 1028
QY 1186 GGGAGAGCGTGGCGGCTTCAACCAAGCTCACAGGCTGACAGCGGCTTTGTGTT 1245
DB 1029 GGGAGAGCGTGGCGGCTTCAACCAAGCTCACAGGCTGACAGCGGCTTTGTGTT 1088
QY 1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGCTCAATCTGAGAGAAAGATTGTC 1305
DB 1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGCTCAATCTGAGAGAAAGATTGTC 1148
QY 1306 CTGAAGCGCTTCTGCGGTATGCTGTGAGGGAAGTGAATAGAACTCAGTGTTCAT 1365
DB 1149 CTGAAGCGCTTCTGCGGTATGCTGTGAGGGAAGTGAATAGAACTCAGTGTTCAT 1208
QY 1366 GGTGACACCTCATGTTTCAAGAGACTCGGGAGTCTGAGTCTCGTCTGTTTCAATG 1425
DB 1209 GGTGACACCTCATGTTTCAAGAGACTCGGGAGTCTGAGTCTCGTCTGTTTCAATG 1268
QY 1426 AACATCCTTCTCCAGACAGGACCTGAGAGAGTCAACCTTCTCAGCTGAGTCTC 1485
DB 1269 AACATCCTTCTCCAGACAGGACCTGAGAGAGTCAACCTTCTCAGCTGAGTCTC 1328
QY 1486 CAGGACTTCTGCGCGCTTGTACTACGTTTGAAGGCGCTGGAATGACGACGCTCTC 1545
DB 1329 CAGGACTTCTGCGCGCTTGTACTACGTTTGAAGGCGCTGGAATGACGACGCTCTC 1388
QY 1546 TGCCCTCTGATGTTAGAGAGACAAAGATTCATGAGCTTTAAACAGGCTTCAT 1605
DB 1389 TGCCCTCTGATGTTAGAGAGACAAAGATTCATGAGCTTTAAACAGGCTTCAT 1448
QY 1606 ATCACTGCTTTGAGAGAACCGTTCCTTTGAGCCCTGAGACGGAAGATGAGAGG 1665
DB 1449 ATCACTGCTTTGAGAGAACCGTTCCTTTGAGCCCTGAGAGGATGAGAGG 1508
QY 1666 CCACTGAGGCTCTGCTGGGCTGTCGCGTTCCTCGGGGAGTGAAGCAAGACTTCTGAC 1725
DB 1509 CCACTGAGGCTCTGCTGGGCTGTCGCGTTCCTCGGGGAGTGAAGCAAGACTTCTGAC 1568
QY 1726 TGGGTCTCTGTTGGGTCAAGACCTTAATGCAACACCCAGAGAGACCTTGACGCG 1785
DB 1569 TGGGTCTCTGTTGGGTCAAGACCTTAATGCAACACCCAGAGAGACCTTGACGCG 1628
QY 1786 TTCCATCTCTTTTCAAGATCTCAAGACAAAGATTTGTTCCTTGGCATTTAAAGCTTC 1845
DB 1629 TTCCATCTCTTTTCAAGATCTCAAGACAAAGATTTGTTCCTTGGCATTTAAAGCTTC 1688
QY 1846 CAAGAAGTGGCTTCCGATTAACAGAACTTGAATGAGATCTTCTGCTGCTC 1905
DB 1689 CAAGAAGTGGCTTCCGATTAACAGAACTTGAATGAGATCTTCTGCTGCTC 1748
QY 1906 CAGCATGTCCTGATTTGGGAAATTCGGGTGATGATCAAAAGGATTTCTCCAAAGAT 1965
DB 1749 CAGCATGTCCTGATTTGGGAAATTCGGGTGATGATCAAAAGGATTTCTCCAAAGAT 1808
QY 1966 GAGTCCGCTGAGGAGATTCCTGAGTCCCTTAAGATGAGGAGATTAAGACCTCATGAG 2025
DB 1809 GAGTCCGCTGAGGAGATTCCTGAGTCCCTTAAGATGAGGAGATTAAGACCTCATGAG 1868
QY 2026 GAGCATGAGGAAATTTCTGCTCATGCTTGGACCAACCACTGCGGACAGCTGAC 2085

Db 1869 GAGCAGTGGGAAAGTTTCTGCTCCATGCTGGCAACCCACCAACCTGCGGACCTGGAC 1928
Qy 2086 CTGGGCAAGCAGCATCTGTGACAGAGCGGCGCATGAGAACCTGTGTGCCAAGCTGAGCAT 2145
Db 1929 CTGGGCAAGCAGCATCTGTGACAGAGCGGCGCATGAGAACCTGTGTGCCAAGCTGAGCAT 1988
Qy 2146 CCGACCTGCAAGATACAGACCTGTGATTTTGAATAATGACAGATTAACCTGTGTGTGAG 2205
Db 1989 CCGACCTGCAAGATACAGACCTGTGATTTTGAATAATGACAGATTAACCTGTGTGTGAG 2048
Qy 2206 CACCTGTGAGAAATGCTATGCGGCAACCGTAACTGAAATGCGCTCAACCTGTGTGTGAG 2265
Db 2049 CACCTGTGAGAAATGCTATGCGGCAACCGTAACTGAAATGCGCTCAACCTGTGTGTGAG 2108
Qy 2266 CACCTGTGAGAAAGATGTAAGATGCGGTGTGAGAGCTTAAACCAACCAAAATGTTTG 2325
Db 2109 CACCTGTGAGAAAGATGTAAGATGCGGTGTGAGAGCTTAAACCAACCAAAATGTTTG 2168
Qy 2326 TTGAGATCTTTGAGGCTGTGATTTGCTGTGATTTGACCCATGCTGTACCTGAGATCTCC 2385
Db 2169 TTGAGATCTTTGAGGCTGTGATTTGCTGTGATTTGACCCATGCTGTACCTGAGATCTCC 2228
Qy 2386 CAATTCCTTAGAGCTCCCGGAGCTGAAATCTGTGAGCGCTGGAGAAAGAGGTGACA 2445
Db 2229 CAATTCCTTAGAGCTCCCGGAGCTGAAATCTGTGAGCGCTGGAGAAAGAGGTGACA 2288
Qy 2446 GACCAAGGAGTAAATGCTCTGATGATGCTCTTGAAGATCTCCAGTGGCGCTGACAGAG 2505
Db 2289 GACCAAGGAGTAAATGCTCTGATGATGCTCTTGAAGATCTCCAGTGGCGCTGACAGAG 2348
Qy 2506 CTGATCTGAGAGAGCTGTGATGACAGCCAGCGGTTGCCAGAGTCTGGCTCAGCCCTC 2565
Db 2349 CTGATCTGAGAGAGCTGTGATGACAGCCAGCGGTTGCCAGAGTCTGGCTCAGCCCTC 2408
Qy 2566 GTGAGCAACCGGAGCTTGAACAACCTGTGCTATTCACCAACAAGCTGGGAGAAAGAGT 2625
Db 2409 GTGAGCAACCGGAGCTTGAACAACCTGTGCTATTCACCAACAAGCTGGGAGAAAGAGT 2468
Qy 2626 GTAATCTAATCTGTGTGATGATGAGGCTTCCCACTGTAGTCTGACAGAGCTGATGCTG 2685
Db 2469 GTAATCTAATCTGTGTGATGATGAGGCTTCCCACTGTAGTCTGACAGAGCTGATGCTG 2528
Qy 2686 AATGATGCACTGTGACAGCGGCTGTGCTGTGCTTTTCTTGCACTTGGCTTATGGGTAA 2745
Db 2529 AATGATGCACTGTGACAGCGGCTGTGCTGTGCTTTTCTTGCACTTGGCTTATGGGTAA 2588
Qy 2746 TCATGCTGAGAGAGCACTGAGGCTTGAAGAACCTGTGTGAGAAACAATGGGTGAAAGCTT 2805
Db 2589 TCATGCTGAGAGAGCACTGAGGCTTGAAGAACCTGTGTGAGAAACAATGGGTGAAAGCTT 2648
Qy 2806 CTGTGCGAGGCTCATGAGAGAAACAATCTGTGATCTCCAGAGCTGAGATGTGTAAAGTGT 2865
Db 2649 CTGTGCGAGGCTCATGAGAGAAACAATCTGTGATCTCCAGAGCTGAGATGTGTAAAGTGT 2708
Qy 2866 CATCTCACCGCGCGGTGTGAGAGTGTCTGTGTGATCTGAGAGAGAGACACCTG 2925
Db 2709 CATCTCACCGCGCGGTGTGAGAGTGTCTGTGTGATCTGAGAGAGAGACACCTG 2768
Qy 2926 AAGAGCTGTGATCTCAAGAGAAATGCTGTGGGTGACGCTGGGTGTGCTGCGCTGTGCGAG 2985
Db 2769 AAGAGCTGTGATCTCAAGAGAAATGCTGTGGGTGACGCTGGGTGTGCTGCGCTGTGCGAG 2828
Qy 2986 GGAATGAGCAAAAGAAACAGTGTCTGAGAGAGCTGGGTTGAAAGGCAATGAGACTGACT 3045
Db 2829 GGAATGAGCAAAAGAAACAGTGTCTGAGAGAGCTGGGTTGAAAGGCAATGAGACTGACT 2888
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Db 2889 TCTGATGCTGTGAGAGCACTCTCTTGGCCCTTTCTGCAACCGGCACTGACAGAGCTTA 2948
Qy 3106 AACCTGTGTGAGAAATTAATTAATGCTCCCAAGAGAAATGATGAAGCTGTGTTGGCCTTTGGC 3165
Db 2949 AACCTGTGTGAGAAATTAATTAATGCTCCCAAGAGAAATGATGAAGCTGTGTTGGCCTTTGGC 3008

Qy 3166 TGTCCAGTCTTAACATTAAGATTAATTTGGCTGTGAAATGAGAGTAACTGTGCAATA 3225
Db 3009 TGTCCAGTCTTAACATTAAGATTAATTTGGCTGTGAAATGAGAGTAACTGTGCAATA 3068
Qy 3226 AGAAAGCTGTGAGAGAAATGCTGAGTCTCAAGCCCGGAGTGTGAAATGAGAGTGTG 3285
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Qy 3286 CATCTTTGATGAGAGTGAACCGGACAC 3312
Db 3129 CATCTTTGATGAGAGTGAACCGGTAC 3155

RESULT 10
US-10-399-443-5
; Sequence 5, Application US/10399443
; Publication No. US2004002869A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-399-443-5

Query Match 31.7%; Score 1278; DB 17; Length 3447;
Best Local Similarity 67.2%; Pred. No. 0;
Matches 1898; Conservative 0; Mismatches 908; Indels 18; Gaps 6;

Qy 498 TGAATGCGCCGGAATGCAAACTTGGCTGTGCTTTGATTCAGACCGTGGGCTCCG 557
Db 515 TGAAGGCCAGAGATGAAATTAATTTGCTGATGCTTTTAAACCATACAGAAACCTTCA 574
Qy 558 GCTTCGACAGGTGTGCTTGCACGGAAGTCAAGAAATGCGGCTTACGACAGAG 617
Db 575 GCTTCACACATTAATCTTACAGAGAGACAGAGAGTGGAGTCAAGCTTTGGCAGAG 634
Qy 618 GATGTGCTGTGCTGGCGCAGAGGTGACTCTACAGGGAATGTTCTCTACGTTCTT 677
Db 635 TATGTCTTGGCTGGGCAAGGCTTAATCTTCCAAAATG---TCTTTGTCACTT 691
Qy 678 CTTCCCGGTGAGAGATGACGCGGAAGAGAGAGAGTCAAGATTCATCTCCAG 737
Db 692 CTTCTCTGTGAGAAATTAAGTGAAGAGAGAGAGAGTGTGCAAGCTGATTTGCTAA 751
Qy 738 GGAATGAGCACTTCCAGGCTCCGCTGACGAGATCATGATCCGACCAAGAAAGCTGT 797
Db 752 GGAATGAGCACTTCCGAGATCTTGTGATCAAAAGATCATGATCCAGCAAGAAAGCTT 811
Qy 798 GTTCATATTAACGCTTTCATGATGACTGTGGCTGTCTCTC---AACATGACAAAGCT 854
Db 812 GTTGTATATATATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 871
Qy 855 CTGCAAGAGCTGGGCTGAGAGAGAGCTCCGTTCAACCTCATACGAGTGTGCTGAGAG 914
Db 872 ATCCAGAGACTGGAAGATGAACAGCCCATATATATCATCTGTATGATGATGATGATGAT 931

QY 915 GATCTGCTCCCTGAGTCTCTTCTGATGTCACCGTCAGAGACGTGGGACAGAGAGCT 974
DB 932 GGCCTCTTACTCTAGTCTCTTCTCATCTTACACAGAGAAACAGAGCTTGAAGAACT 991
QY 975 CAAGTCAGAGGTGCTGTCTCCCGCTTACCTGTAGTGAAGAACTCCGGGAAACAAAG 1034
DB 992 CAAGTCAGAGGTGCTGTCTCCCGCTTATATAGTGTGAAGAACTGTCTGATCAAGAG 1051
QY 1035 AATCACTTGTCTCTTGAAGCCGGGATGTGTAGATCAAGAAACAGAGGTTGCTGTC 1094
DB 1052 ATCTCAGCTGTGCTCTGAGAAATCTCCAAATGATCTGATGAATACAAAGTCTTCATTC 1111
QY 1095 GATCATGAACAACGTCGAGCTGTCGACAGTCCAGAGTCCCGGCTGAGCTCTCAT 1154
DB 1112 TCTGATGAAGAAATCACAGCTGTCTTGAACCAATGACAGGCCCTCTGTGTGCTCTGCT 1171
QY 1155 CTGCGTGGCCCTGACAGTCGACAGAGCGTGTGGGAGAGCGTCCGCCCTTCAACCAAC 1214
DB 1172 CTGTGAGGCTCTACAGCTTACAGAAAGAACTGGGAAAGAGATGACCTTACCTGACAGC 1231
QY 1215 GCTCAGAGGCTGACAGCGGCTTGTGTCTTATCAGCTCACCCCTCAGAGCGTGTGCTG 1274
DB 1232 TCTCAGCGGTTGTATGTCAGCTGTGTCTTCAACAGCTCACCTTGAAGAGCTTCCCA 1291
QY 1275 GCGCTGCTCAATCTGAGAGAAAGTGTCTGAAAGGCTTCTGCGATGTGCTGTGGA 1334
DB 1292 GAGGCTCTCAGTCAAGAGAAACAGATTACTGTAGGTGTGTGATGATGAGGACGTGA 1351
QY 1335 GAGAGTGTGAATAGAGAGTCAAGTGTGTGATGTGACACATCATGTGTCAAGAGCTGG 1394
DB 1352 AGAGTGTGACCAAGAGT 1411
QY 1395 GAGAGTGTGAGTCTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1451
DB 1412 GAGAGTGTGAGTCTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1471
QY 1452 TGAGAGATCTACACCTTCTTCCACATGATCTCAGAGCTTCTGCGTGTGCTGTGATCA 1511
DB 1472 TGAGAGATCTTATGT 1531
QY 1512 CGTGTGTGAGAGGCTGTGAATTCAGAGCACTCTGCGCTCTGTGATGTGAAGAGACAA 1571
DB 1532 TGTGTGTGAGAGGCTGTGA---GGAATGGAATCAGATTTGTGTGTGTGTGTGTGTGT 1588
QY 1572 GAGGTCAATGAGCTTAAACAGGAGGCTTCCATATCACTGCTGTGTGTGTGTGTGTGT 1631
DB 1589 GAGGTCAATGAGGCTGAGAGAGATGACGACACTGCTGCTC---CTGGGATGAAAGCTTT 1645
QY 1632 CTGTGTGTGCTCTGAGAGAGAGATGAGAGGCTCAGAGGCTGTGCTGGGCTGTCC 1691
DB 1646 CTGTGTGTGCTCTGAGAGAGATGAGAGATGAGAGGCTGTGAGAGGCTGTGTGTGTGT 1705
QY 1692 CGTTCCTGCGGGGTGAAGAGAGCTTCTGCACTGGGCTCTCTGTGTGTGTGTGTGTGTGT 1751
DB 1706 CGTGTGTGCACTGTGTGAGAGAGCTTCAACACTGGGCTCTCTGTGTGTGTGTGTGTGT 1765
QY 1752 TAAATGCAACACCCAGAGAGACCTGAGCGCTTCACTGTCTTGTGTGTGTGTGTGTGT 1811
DB 1766 CAATGAGCAACAGCCCAATGAGACCTGTGATGCTTCAATGTGTGTGTGTGTGTGTGT 1825
QY 1812 CAAGAAGT 1871
DB 1826 TGAAGAAGT 1885
QY 1872 GAACCTGAGCTTGAATAGATCTTCTCTGCTCTCAGAGCTGTCCGTATTTGTGTGTGTGT 1931
DB 1886 GAAGTGTGATTTGAAGGTCTCTTCTTACTGTCTCAAGACCTGTGTGTGTGTGTGTGTGT 1945
QY 1932 TCGGCTGT 1991
DB 1946 CCGGCTGT 2005

QY 1992 CCCTCTATGATGTCGGGA---TAAAGCCCTCATTTGAGAGAGAGTGGAGAAATTTGTGCTC 2048
DB 2006 TACTGTCCAGAGAGACAGATGTAAAGCCCTCTCTCATGAGGTGTGGGAAACTTGTGCTC 2065
QY 2049 CATGCTGTGCAACCCACCAACCTGCGGAGTGTGAGCTGTGGCAGAGATCTGTACAGA 2108
DB 2066 TGTGCTGTGCAAGCTCTCCGAACTTGAAGAGCTGTGAGCTTGTGGGACAGATCTGTGCTCA 2125
QY 2109 GCGGCTGTGAGAGACCTGTGTGTGCAAGCTGAGGATCCACCTGACAGATACAGACCT 2168
DB 2126 ACGGCTGTGAGAGATCTGTGTGTGCTGAGCTGTGGAGATGATCTGTGAGATACAGAGCT 2185
QY 2169 GATGTTTGAATGACAGATTAACCTGTGTGTGAGAGACCTGTGAGATGTATGTGC 2228
DB 2186 GACGTTTGAAGTGTGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2245
QY 2229 CAACCTGTACCTTGAATCTGTACCTTGTGAGAGACCACTGTGAAGAGAGATGTAG 2288
DB 2246 CAATCAAACTTAAAGTACTCAATCTAGGAGACCTCCATGAGAGATGATGATGA 2305
QY 2289 GATGCGGTGTGAGGCTTAAACACCCAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
DB 2306 GTTGTGCTGTGAGAGGCTGAAACATTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2365
QY 2349 CTGTGATTTGACCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2408
DB 2366 CTGTGATTTGACCCATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2425
QY 2409 CCGTAATCTGTAGCTGTGAGAGAGAAACAGGTGTGACAGAGGATATGCTGTGTGT 2468
DB 2426 GCTAAAGT 2485
QY 2469 TGT 2528
DB 2486 GATGCTGT 2545
QY 2529 CACAGCAAGGTTGTGAGAGT 2588
DB 2546 CACAGCTGT 2605
QY 2589 CCGTGTCTATTCACACAGCTGTGGGAGAGAGGTGTAAATCTGTGTGTGTGTGTGTGT 2648
DB 2606 CCGTGTCTATTCACACAGCTGTGGGAGAGAGGTGTAAATCTGTGTGTGTGTGTGTGT 2665
QY 2649 GAGGCTGT 2708
DB 2666 GAGGATCTGAGATGT 2725
QY 2709 TGGCTGT 2768
DB 2726 TGT 2785
QY 2769 TAGCATGAACCTGTGTGAGAGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2828
DB 2786 GACCATGAACCCCGTAGGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2845
QY 2829 ATCTGT 2888
DB 2846 TACTGT 2905
QY 2889 GAGT 2948
DB 2906 GAGCTGT 2965
QY 2949 TGCCCTGT 3008
DB 2966 GCGCTGT 3025
QY 3009 TGT 3068
DB 3026 CCGT 3085
QY 3069 CTGTGCGCTTCTGT 3128

Accession	Sequence	Position
D8	ATTGGCCATCTTGGCAACCTCACTTAACAGCTTAACCTGGTGAAGAAATGACTTCAG	3145
QY	TCCCAAGAAATGATGAAGAGCTGTGTTGGGCTTTGGCTGTGCCAGCTTAACTTACAGAT	3188
D8	TACATCGGGGATGTTGAAGCTGTGCTGCCTTCCAAATGCCCTGTCTCTAACTCGGGGAT	3205
QY	AATTGGGCTGTGGAATAATGGCAGTACCTGTGCTCAATAATAGGAAGCTGTGAGAGAAAGTCA	3248
D8	AATTGGCTGTGGAAGCAGAGATCTAATGCCGAGTGAAGAAAGACGCTGGAGGAATTGA	3265
QY	GCTACTCAAGCCCCGAGTCGTAAATGAAGGTAGTGGCATCTTTTATGTAAGATGACCG	3308
D8	GTTTGTCAGGCCCACTGTGATTAAGATGATGATTTGTATGCTATGATGTAAGATGACCG	3325
QY	ACAC	3312
D8	AAAC	3329

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RESULT 11
US-10-677-943-5
/ Sequence 5, Application US/10677943
/ Publication No. US20040072297A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
APPLICANT: represented by the Secretary of the Department of Health and
APPLICANT: Human Services
APPLICANT: Nelson, Lawrence
APPLICANT: Tong, Zhi-Bin
TITLE OF INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64790
CURRENT APPLICATION NUMBER: US/10/677,943
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: 60/241,510
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US02/09776
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 3447
TYPE: DNA
ORGANISM: Mus musculus
US-10-677-943-5

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Query Match	31.7%	Score 1278;	DB 17;	Length 3447;
Beet Local Similarity	67.2%;	Pred. No. 0;		
Matches 1898;	Conservative	0;	MisMatches 908;	Indels 18; Gaps 6;
Qy	498	TGAC	TGGGCGGAAATGCAAAAGCTGGTGGCGTGGGCTTTTCATTTCAGACGGGTGGGGCTTCGG	557
Db	515	TGACAGCCCAAGATGAATTAATTTATGTCTGAATGCTTTTAAACATACAGAAACCTTTTCA	574	
Qy	558	GCTTCGACGGTGGTTTTCGACACGGAAATCAGAAATGGGAAATCGGCTTCAGCAGAG	617	
Db	575	GCTTCACACCATTTATTCACATGGAAGACAGAGATTGGAAAGTACGTTTGGCCAGAG	634	
Qy	618	GATCGTGTGTGTGGGCGCAAGGTGAAGCTTACACGGAATGTTCCTACGTTCTT	677	
Db	635	TATGTTCCTTGGCTGGGACAGGGTAAACTCTTCCAAAAAATG---TCTTTGTATCTT	691	
Qy	678	CCTCCCGCTTAGAAGATGACAGCGGAAAGAAAGACAGTGTCAAGATTCATCTCAG	737	
Db	692	CTTCTCTGTGAGAAATTAAGATGACAGAAAGGCAATTGGCAGCGTGAATTGCTAA	751	
Qy	738	GGAGTGGCAGACTCCACAGGCTCCGGTACAGGAAGATCATGTCGCCAGCAGAAAGGCTGT	797	
Db	752	GGAGTGTCAAGACTCTCGGGATCTAATGACAAAGTCAATGTCCCAACAGAAAGACTTCT	811	
Qy	798	GTTTCATCATTTGACGGTTTCGATGACCTGGGCTGTCTC---AACAATGACAAAGCT	854	

Db	812	GTTTGTCAATAGATGCTTGGATGATAGCATCTGTCTCTCCAACTGATGTATGACACT	871
OY	855	CTGCAGAAAGCTGGGCTGAGAGACAGCCTCCGTTACACCTCATACGACAGTCTGTAGGAA	914
Db	872	ATCCAGAGACTGGAGAGATGAACAGCCCATATCATCTGATGTACAGCCTCTGAGGAA	931
OY	915	GGTCTCTGCTCCCTGAGTCTTTCGTGATGTCAACGCTCAAGACGTGGGCAAGAAAGCT	974
Db	932	GGCTCTCTTACCTCAAGTCTTTCATCATATTAACACAGAAACAAGGCTTAGAAAACT	991
OY	975	CAAGTCAGAGGTCTGTCTCTCCCGTTACTGTATGAGGAATCTCCGGGAAACAAG	1034
Db	992	CAAGTCATGTGTGTGTCTCCCTCTATATATCTGTTGAAGAGCTGTCTGATCAAGAG	1051
OY	1035	AATCCACTGTCTCTTGAAGCGGGGAATTGGAGCATATCAAGAAACAAGGGTTGGCGC	1094
Db	1052	ATCTCAAGTGTCTCTCGAAGAAATCTCCATATGATGTATGAAATACAGTCTTCATTC	1111
OY	1095	GATCATGAACAACCGTAGCTCTCGACAGATGCAAGTGCAGGTGCGCGCGCTCTCAT	1154
Db	1112	TCTGTATGAATAATACCAAGCTGTTTGAACAAATGCAAGGCCCTCTGTGTCTCCGTGT	1171
OY	1155	CTGCGTGCCCTGCAAGCTGCGAGACGTGTGTGGGGAAGCGTCCGCCCTTCAACCAAC	1214
Db	1172	CTGTAGGCTCTCAAGCTACAGAAAGAACTGGGAAAGAGATGACCTTACCTCCAGAC	1231
OY	1215	GCTCAACAGGCTGAGCGCGCTTTTGTGTTTCATCAGCTCAACCCCTCGAGGCGTGTCCG	1274
Db	1232	TCTCAACGCTTGTATGTCCAGCTGTGTGTTCACACAGCTCACTTGAAGAGGCTTCCCA	1291
OY	1275	GCAGCTGTCAATCTGAGAGAAAGATTTCTTGAAGCGCTTCTCCGTAATGCTGTGA	1334
Db	1292	GAGGCTCTCAGTCAAGGAAGAACAGATTACTCTAGTGGGTTTGTGATGATGGCAGCTGA	1351
OY	1335	GCGAGTGTGAATAGGAAGTCAAGTGTGTGATGTGAAGACCTCATGTGTTCAAGACTCGG	1394
Db	1352	AGGAGTGTGACATAGAGTGTGTGTCTATAGATGAATGACCTGAAGAACTATTAACCTTAA	1411
OY	1395	GGAAGTCAGAGTCCAGTGTCTGTGTTTCAATGAATATCTTCCACAGAGC---ACTG	1451
Db	1412	GGAAGTCAGAGTCTTGGCCCTTTCACATGAACATCTTCTTCCAGGTGGCCACACAG	1471
OY	1452	TGAGAGATACACACTTCTTCAACTCAGTCTCAAGACCTTCTGTGCGGCTTGTACTA	1511
Db	1472	TGAGCAGTGTATGTTTCTTCCCACTCAAGCTGCAAGATTTCTTGTGTCTTATATTA	1531
OY	1512	CTGTGTAGAGGCGCTGGAATTCAGACCAAGCTCTGTGCCCTGTGACGTTGAGAAACAA	1571
Db	1532	TGTTTATGAGGGGCTGGA---GGAATGGAATCAGCAATTTTGTCTCAATTGAAACCAAG	1588
OY	1572	GAGGTCCATGAGGCTTAAACAGGAGGCTTCCATATCACTCGCTTGGATGAAGCGTT	1631
Db	1589	GAGCATCATGAGGATGAAGAACTGACAGACTGCGCTC--CTCGGATGAAGCGTT	1645
OY	1632	CTGTGTGAGCTCTGTGACGGAAGACGTAAAGAGGCGCACTGGAGGCTCTGTCTGAGCTGC	1691
Db	1646	CTTATTTTGGCTCATGAACAAGATATCTTGAAACATCTGGAAGTTTCTGTTTGAATATCC	1705
OY	1692	CGTTCCCTGGGGGTGAAGCAGAAAGCTTCTGCACTGGGTCTCTGTGTGGTCAAGACC	1751
Db	1706	CGTATTTCAACTGTGTAGCAGAAAGCTCAACACTGGGATCTCTCTGATAGCTCAGAGGT	1765
OY	1752	TAAATGCCACCCCAAGAGACACCCCTGAGACGCTTTCATCTTTTTCAGAGACTCAAGA	1811
Db	1766	CAATGGAACCAAGCCCAATGACACCCCTGAGAGCTTCTTATTTGTCTATTTTGAATCTCAGA	1835
OY	1812	CAAGAAGTTTGTGCTTGGCATTAACAAGCTTCCAAAGATGTGGCTTCGATTAACA	1871
Db	1826	TGAAGAGTTTGTGGCGGGGCTCTCAACGCTTCCAAAGATGTGGCTGCTGATTAACA	1885
OY	1872	GAACTGGACTGTATAGACTTCTTCTGTGCTCAGACACTGTCCGTAATTTGCGGAAAT	1931

QY 994 CCCCCTTACCTGTTAGTTAGAGAAATCTCCGGGGAAACAAGAAATCCATTGCTCCTTGAG 1053
Db 241 CCCCCTTACCTGTTAGTTAGAGAAATCTCCGGGGAAACAAGAAATCCATTGCTCCTTGAG 300
QY 1054 CCGGGGATTGGTGACATCAGAAACAACAAGGTTGGTGACATCAGAAACAACCGTGAG 1113
Db 301 CCGGGGATTGGTGACATCAGAAACAACAAGGTTGGTGACATCAGAAACAACCGTGAG 360
QY 1114 CTGCTCGACCAAGTCCAGAGTCCCGCGTGAGCTCTCATCTGCGAGCCCTGCACTG 1173
Db 361 CTGCTCGACCAAGTCCAGAGTCCCGCGTGAGCTCTCATCTGCGAGCCCTGCACTG 420
QY 1174 CAGGACGTGGGGGAGAGAGCTGCGCCCTTCAACCAACGCTCAACAGCTGCAAGCC 1233
Db 421 CAGGACGTGGGGGAGAGAGCTGCGCCCTTCAACCAACGCTCAACAGCTGCAAGCC 480
QY 1234 GCTTTTGTTGTTTATTCAGCTCAACCCCTGAGAGCGTGCGCGCTGCTCAATCTGAG 1293
Db 481 GCTTTTGTTGTTTATTCAGCTCAACCCCTGAGAGCGTGCGCGCTGCTCAATCTGAG 540
QY 1294 GAAAGATTGTCCTGAGACGCTTCTGCGGTATGGCTGAGAGGAGTGTGAAATAGAGAG 1353
Db 541 GAAAGATTGTCCTGAGACGCTTCTGCGGTATGGCTGAGAGGAGTGTGAAATAGAGAG 600
QY 1354 TCAGTGTTTGATGATGAGAGACCTCATGAGTTCAAGAACTCGGGAGTCTGAGCTGCT 1413
Db 601 TCAGTGTTTGATGATGAGAGACCTCATGAGTTCAAGAACTCGGGAGTCTGAGCTGCT 660
QY 1414 CTGTTTCAATGAAATCTCTTCTCCCAAGACCACTGTGAGAGTACTACCTTCTTC 1473
Db 661 CTGTTTCAATGAAATCTCTTCTCCCAAGACCACTGTGAGAGTACTACCTTCTTC 720
QY 1474 CACCTCAGTCTCAGAGCTTCTGTGCGCGCTTGTACTAGTGTAGAGAGGCTGGAATC 1533
Db 721 CACCTCAGTCTCAGAGCTTCTGTGCGCGCTTGTACTAGTGTAGAGAGGCTGGAATC 780
QY 1534 GAGCGAGCTCTGCGCTCTGTACGTTGAGAAACAAGAGTCCATGAGCTTAAACAG 1593
Db 781 GAGCGAGCTCTGCGCTCTGTACGTTGAGAAACAAGAGTCCATGAGCTTAAACAG 840
QY 1594 GCGAGCTTCCATATCCATCTGCTTGTGAGTGAAGAGTCTTGTGAGGCTGTGAGAG 1653
Db 841 GCGAGCTTCCATATCCATCTGCTTGTGAGTGAAGAGTCTTGTGAGGCTGTGAGAG 900
QY 1654 GACGTAAAGAGAGCACTGAGAGGTCGTGCGGTGTCGCCCTGCGGGGTGAAGAG 1713
Db 901 GACGTAAAGAGAGCACTGAGAGGTCGTGCGGTGTCGCCCTGCGGGGTGAAGAG 960
QY 1714 AAGCTTTCGACCTGGGTCTCTGTGTTGGTTCAGAGGCTTAATGCAACCCAGAGAG 1773
Db 961 AAGCTTTCGACCTGGGTCTCTGTGTTGGTTCAGAGGCTTAATGCAACCCAGAGAG 1020
QY 1774 ACCCTGAGACGCTTCCATCTGCTTGTGAGACTCAAGACAAAGAGTTGTTGCTTGCA 1833
Db 1021 ACCCTGAGACGCTTCCATCTGCTTGTGAGACTCAAGACAAAGAGTTGTTGCTTGCA 1080
QY 1834 TTAAACAGCTTCCAAAGAGTGGCTCCGATTAACCAAGAGCTGAGCTTGATAGCACT 1893
Db 1081 TTAAACAGCTTCCAAAGAGTGGCTCCGATTAACCAAGAGCTGAGCTTGATAGCACT 1140
QY 1894 TCCTTTCGCTCCAGC 1909
Db 1141 TCCTTTCGCTCCAGC 1156

RESULT 13
US-10-677-943-1

; Sequence 1, Application US/10677943
; Publication No. US20040072297A1

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and

; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Query Match 28.6%; Score 1152.8; DB 17; Length 1157;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 754 CAGGCTCCGGTGACGAGATCATGTCCGACCAAGAAAGCTGTTTCAATCATGACGGT 813
Db 1 CAAGCTCCGGTGACGAGATCATGTCCGACCAAGAAAGCTGTTTCAATCATGACGGT 60
QY 814 TTCAATGACCTGGGCTGTGCTTCTCAACAAATGACCAAAAGCTGCGAAAGCTGGGCTGAG 873
Db 61 TTCAATGACCTGGGCTGTGCTTCTCAACAAATGACCAAAAGCTGCGAAAGCTGGGCTGAG 120
QY 874 AAGGAGCTCCGTTCAACCTCATATGAGAGTCTGCTGAGAAAGTCTGCTCCCTGAGTCC 933
Db 121 AAGGAGCTCCGTTCAACCTCATATGAGAGTCTGCTGAGAAAGTCTGCTCCCTGAGTCC 180
QY 934 TTCTGATGCTCACGCTCAAGAGAGTGGGCAACAGAAAGCTCAAGTCAAGAGTGTGCT 993
Db 181 TTCTGATGCTCACGCTCAAGAGAGTGGGCAACAGAAAGCTCAAGTCAAGAGTGTGCT 240
QY 994 CCCCCTTACCTGTTAAGTTAAGAGAAATCTCCGGGGAAACAAGAAATCCATTGCTCCTTGAG 1053
Db 241 CCCCCTTACCTGTTAAGTTAAGAGAAATCTCCGGGGAAACAAGAAATCCATTGCTCCTTGAG 300
QY 1054 CCGGGGATTGGTGACATCAGAAACAACAAGGTTGGTGACATCAGAAACAACCGTGAG 1113
Db 301 CCGGGGATTGGTGACATCAGAAACAACAAGGTTGGTGACATCAGAAACAACCGTGAG 360
QY 1114 CTGCTCGACCAAGTCCAGAGTCCCGCGTGAGCTCTCATCTGCGAGCCCTGCACTG 1173
Db 361 CTGCTCGACCAAGTCCAGAGTCCCGCGTGAGCTCTCATCTGCGAGCCCTGCACTG 420
QY 1174 CAGGACGTGGGGGAGAGAGCTGCGCCCTTCAACCAACGCTCAACAGGCTGCAAGCC 1233
Db 421 CAGGACGTGGGGGAGAGAGCTGCGCCCTTCAACCAACGCTCAACAGGCTGCAAGCC 480
QY 1234 GCTTTTGTTGTTTATTCAGCTCAACCCCTGAGAGCGTGCGCGCTGCTCAATCTGAG 1293
Db 481 GCTTTTGTTGTTTATTCAGCTCAACCCCTGAGAGCGTGCGCGCTGCTCAATCTGAG 540
QY 1294 GAAAGATTGTCCTGAGACGCTTCTGCGGTATGGCTGAGAGGAGTGTGAAATAGAGAG 1353
Db 541 GAAAGATTGTCCTGAGACGCTTCTGCGGTATGGCTGAGAGGAGTGTGAAATAGAGAG 600
QY 1354 TCAGTGTTTGATGATGAGAGACCTCATGAGTTCAAGAACTCGGGAGTCTGAGCTCGT 1413
Db 601 TCAGTGTTTGATGATGAGAGACCTCATGAGTTCAAGAACTCGGGAGTCTGAGCTCGT 660
QY 1414 CTGTTTCAATGAAATCTCTTCTCCCAAGACCACTGTGAGAGTACTACCTTCTTC 1473
Db 661 CTGTTTCAATGAAATCTCTTCTCCCAAGACCACTGTGAGAGTACTACCTTCTTC 720

QY	1474	CACCTCAAGCTCCAGAACTTCTGTGCGGCTTGTACTAGTGTAGAAGGACCTGGAAATC	1533
Db	721	CACCTCAAGCTCCAGAACTTCTGTGCGGCTTGTACTAGTGTAGAAGGACCTGGAAATC	780
QY	1534	GAGCCAGCTCTCTGCGCTCTGTAGCGTTGAGAAACAAGAGTCCATGAGCTTTAAACAG	1593
Db	781	GAGCCAGCTCTCTGCGCTCTGTAGCGTTGAGAAACAAGAGTCCATGAGCTTTAAACAG	840
QY	1594	GCAGGCTTCCATATCACTGCGTTTGGAAAGACGTTTCTTGTGGCCCTCGTAGGCGGA	1653
Db	841	GCAGGCTTCCATATCACTGCGTTTGGAAAGACGTTTCTTGTGTGCGCTCGTAGGCGGA	900
QY	1654	GACGTGAAGAGGCCACTGAGAGTCTGTGCGGCTGTCCCGTTCCCTCGGAGGTGAAGCAG	1713
Db	901	GACGTGAAGAGGCCACTGAGAGTCTGTGCGGCTGTCCCGTTCCCTCGGAGGTGAAGCAG	960
QY	1714	AAAGCTTCGCACTGGGTCTCTCTGTGGGTCAAGACGCTAATAGCCAACACCCAGAGAC	1773
Db	961	AAAGCTTCGCACTGGGTCTCTCTGTGGGTCAAGACGCTAATAGCCAACACCCAGAGAC	1020
QY	1774	AACCTGAGAGGCTTGCACATGTCTTTTCGAGACTCAAGACAAGAGTTTGTTCGCTTGCA	1833
Db	1021	AACCTGAGAGGCTTGCACATGTCTTTTCGAGACTCAAGACAAGAGTTTGTTCGCTTGCA	1080
QY	1834	TTAAACAGCTTCCAAAGAGTGTGCTTCGATTTAACAGAACCTTGACTTGAATAGCATCT	1893
Db	1081	TTAAACAGCTTCCAAAGAGTGTGCTTCGATTTAACAGAACCTTGACTTGAATAGCATCT	1140
QY	1894	TCCTTCGCTCCAGC	1909
Db	1141	TCCTTCGCTCCAGC	1156

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RESULT 14
US-10-399-443-3
Sequence 3, Application US/10399443
Publication No. US20040028669A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary, Department of Health & Human Services, The National Institute
APPLICANT: Health
APPLICANT: Nelson, Lawrence M.
APPLICANT: Tong, Zhi-Bin
APPLICANT: Nelson, Lawrence
APPLICANT: Zhi-Bin, Tong
TITLE OF INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64785
CURRENT APPLICATION NUMBER: US/10/399,443
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/241,510
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1075
TYPE: DNA
ORGANISM: Homo sapiens
US-10-399-443-3

Query Match      18.8%; Score 756.6; DB 17; Length 1075;
Best Local Similarity 99.5%; Pred. No. 1.3e-215;
Matches 759; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      2550  TCTGGCCTCAGCCCTGTCGACGCAACCGAGCTTGACACACCTGTGCTATCCACAACAG 2609
Db      1      TCTGGCCTCAGCCCTGTCGACGCAACCGAGCTTGACACACCTGTGCTATCCACAACAG 60

Oy      2610  CCTGGGGAGCAAGAGTGAATCTACTGTGTGATCCATAGAGCTTCCCACTGTAGTCT 2669
Db      61      CCTGGGGAGCAAGAGTGAATCTACTGTGTGATCCATAGAGCTTCCCACTGTAGTCT 120

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QY	2670	GCAGAGGCTGATGCTGAATCAGTGCACCTTGACAACGGCTGGCTGTGTTTCTTGCACT	2729
Db	121	GCAGAGGCTGATGCTGAATCAGTGCACCTTGACAACGGCTGGCTGTGTTTCTTGCACT	180
QY	2730	TGCGCTTAATGSGTAACTCATGAGCTGACGACCTGAGCCTTAGCATGAACCTGTGGAAGA	2789
Db	181	TGCGCTTAATGSGTAACTCATGAGCTGACGACCTGAGCCTTAGCATGAACCTGTGGAAGA	240
QY	2790	CAATGAGCGTGAAGCTTCTGTGACGAGTGCATGAGAGAAACAATCTTGATCTCCAGGACCT	2845
Db	241	CAATGAGCGTGAAGCTTCTGTGACGAGTGCATGAGAGAAACAATCTTGATCTCCAGGACCT	300
QY	2850	GGAAGTGGTAAAGTGCATCTCACCGCGCGTGCCTGTGAGAGTCTGTCTGTGTGATCTC	2900
Db	301	GGAAGTGGTAAATATATATCTCACCGCGCGTGCCTGTGAGAGTCTGTCTGTGTGATCTC	360
QY	2910	GAGAGACGACACCTGAAAGACCTGAGATCTCACCGACAAATGCCCTTGSGTACCGTGGCGT	2965
Db	361	GAGAGACGACACCTGAAAGACCTGAGATCTCACCGACAAATGCCCTTGSGTACCGTGGCGGT	420
QY	2970	TGCTGCGCTGTGCGAGGGGACTGAAGACAAAAGACAGTGTTCGACGAGACTCGGGTTGAA	3025
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QY	3030	GGCATGTGGACTGATCTGTGATTCCTGTGAGGCACTCTCCTTGGGCCCTTTCCTGCACCG	3089
Db	481	GGCATGTGGACTGATCTGTGATTCCTGTGAGGCACTCTCCTTGGGCCCTTTCCTGCACCG	540
QY	3090	GCATCTGACCAAGTCTTAAACCTGTGTGCAGAAATTAATTCAAGTCCCAAGAAATGAATGAAGCT	3145
Db	541	GCATCTGACCAAGTCTTAAACCTGTGTGCAGAAATTAATTCAAGTCCCAAGAAATGAATGAAGCT	600
QY	3150	GTTGTTGGCCCTTTCGCTGTGCCAGTCTTAACTTAAACAGATTAATTTGGGCTGTGTGAATGGCA	3209
Db	601	GTTGTTGGCCCTTTCGCTGTGCCAGTCTTAACTTAAACAGATTAATTTGGGCTGTGTGAATGGCA	660
QY	3210	GTAACCTGTGCAATTAAGAAAGCTGTGTGAGAGAAATGCACTTCAAGCCCCGAGTCTGT	3265
Db	661	GTAACCTGTGCAATTAAGAAAGCTGTGTGAGAGAAATGCACTTCAAGCCCCGAGTCTGT	720
QY	3270	AATTGAGCGTATGGGCAATCTTTTGAATGAAGATGACCGGATAC 3312	
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US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/09981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-3

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Perfect score: 1344

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1006	74.9	3926	15	US-10-216-645-1
5	988	73.5	3830	15	US-10-216-645-3
6	968	72.0	3226	17	US-10-092-900A-347
7	616	45.8	3885	18	US-10-860-761-3
8	616	45.8	3900	17	US-10-399-443-23
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20	12	0.9	3108	18	US-10-781-294-23
21	12	0.9	3186	14	US-10-124-498-17
22	12	0.9	3186	14	US-10-066-521-17
23	12	0.9	3218	17	US-10-407-866-67
24	12	0.9	3447	17	US-10-399-443-5
25	12	0.9	3447	17	US-10-677-943-5
26	12	0.9	3466	17	US-10-108-260A-718
27	12	0.9	4931	15	US-10-028-374-1
28	12	0.9	4931	16	US-10-183-770-1
29	10	0.7	610	17	US-10-424-599-139217
30	9	0.7	240	16	US-10-029-386-16506
31	9	0.7	270	11	US-09-922-293-1943
32	9	0.7	339	18	US-10-437-963-19943
33	9	0.7	346	18	US-10-425-115-150063
34	9	0.7	394	18	US-10-425-115-72548
35	9	0.7	426	18	US-10-674-124A-25173
36	9	0.7	438	18	US-10-357-930-38072
37	9	0.7	440	17	US-10-424-599-35497
38	9	0.7	564	16	US-10-029-386-2806
39	9	0.7	578	10	US-09-764-891-1745
40	9	0.7	693	18	US-10-363-345A-27001
41	9	0.7	693	18	US-10-363-345A-27002
42	9	0.7	693	18	US-10-363-345A-27115
43	9	0.7	693	18	US-10-363-345A-27116
44	9	0.7	720	13	US-10-027-632-150437
45	9	0.7	720	17	US-10-027-632-150437

ALIGNMENTS

RESULT 1
US-10-124-498-5
Publication No. US20030017983A1
GENERAL INFORMATION:
APPLICANT: Wang, Weiye
APPLICANT: Blatcher, Maria
TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
FILE REFERENCE: 07334-367001
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US/10/124,498
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/318,645
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/265,231
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 25

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; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4032)
US-10-124-498-5

Alignment Scores:
Pred. No.: 0 Length: 4035
Score: 1344.00 Matches: 1344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrglyLeuGlnTrpCysLeuTyrglu 20
DB 1 ATGAGAGAGAGCAAAATGCTCACCTTTCCAGCTAACGGGCTGCAATGGTGTCTTAAG 60
QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysSerSerGluSer 40
DB 61 CTAGACAAAGAAAGATTTCAGACATTCAAGAAATTACTAAAGAAATTCTTCAGAAATCG 120
QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnValaGluCysLeuAlaLeu 60
DB 121 ACCACATGCTTATTCCACAGATTGGAATCGAAGATCGAACCTGGATGCTGGCACTC 180
QY 61 LeuLeuHisGluTyrglyTyrglyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
DB 181 CTCTGATGAGATATTATGAGACATCGCTGGCTGGGCTGATCATTAAGCATCTTGAA 240
QY 81 AsnMetAsnLeuAgtThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
DB 241 AACATGAACCTGCACCACTCTCGAAGAAAGCAGCGGATGACATGAATAAAATTTCNA 300
QY 101 AlaMetGluGlnGluGluAlaThrAlaAlaGluThrGluGlnGluIleSerGlnAla 120
DB 301 GCTATGAAACAAAGAGTGCACACGACACAGACAGAAACAGAAATTTCCACAGCT 360
QY 121 MetGluGlnGluGluAlaThrAlaAlaGluThrGluGlnGluIleGluTyrglyAspThr 140
DB 361 ATGAAACAAGAGAGTGCACAGCAGCAGAGACAGAAACAGAACATGGAGGACACA 420
QY 141 TrpAspTyrglySerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
DB 421 TGGACCTACAAAGAGTCACTGTATGACCAAAATTCCTGAGGAGGATGTACGTCTAGT 480
QY 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGluAlaPheAspSer 180
DB 481 TTGAAACACATGCTGCTGACGTGCGGAAATGCAAGGTGGCTTGATTTGATTTCA 540
QY 181 AspArgTrpGlyPheArgProArgThrValValLeuHisGluLysSerGlyIleGlyLys 200
DB 541 GACCGGTGGGCTTCGCGCTCGCACGGGTGTTCTGCACGGAAGTCAAGAAATGGGAAA 600
QY 201 SerAlaLeuAlaArgGluLeuValLeuCysTrpAlaGlnGluGlyLeuTyrglyMet 220
DB 601 TCGGCTCTAGCAAGAGATCGTCTGTGCTGGCGCAGAGGTGACCTTACCAAGGAAATG 660
QY 221 PheSerTyrglyAlaPhePheLeuProValArgLysMetGlnArgLysLysGluSerSerVal 240
DB 661 TTCTCTACGTTCTTCTCTCCCGTTAGAGAGATGACGCGAAGAAAGAGACAGTGC 720
QY 241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
DB 721 ACAAGATTCAATCTCCAGGAGTGGCCAGACTCCACAGGCTCGGATGACGAGATATATGCC 780
QY 261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
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DB 781 CGACCAAGAAAGCGCTGTTTATTAAGAGCTTTCATGACCTGGGCTGTCTTCAAC 840
QY 281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProPheThrLeuIleArg 300
DB 841 AATGACCAAAAGCTCTCCAAAGACTGGGCTGAGAGAGAGCTCGCTTCAACCTCATAGCC 900
QY 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
DB 901 AGTCTGTGAGAGAGTCTGCTCCCTGAGCTCTTCTGATCTGTCACCGTCAGAGAGCTG 960
QY 321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrglyLeuLeuValArgGlyIle 340
DB 961 GGCACAGAGAACTCAAGTCAAGAGTGTGTCTCCGTTACCTGTTAGTGAAGAAATC 1020
QY 341 SerGlyGluGlnArgGluIleHisLeuLeuLeuGluLysGluIleGluGluHisGlnLysThr 360
DB 1021 TCCGGGAAACAAAGAAATCCACTTCTCTTGAAGCGCGGATGGTGAAGCATCAGAAACA 1080
QY 361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
DB 1081 CAAGGTTGGCGTGCATCATGAACAACCGTGAAGCTGTCCACAGTCCAGTCCAGTCCGCC 1140
QY 381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyLysSerValAla 400
DB 1141 GTGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 401 ProPheAsnGlnThrLeuThrGlnTyrglyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
DB 1201 CCTTCAACCAAAAGCTCACAGGCTGTCACGCGCTTTGTGTTTCAATCAGCTCACCCCT 1260
QY 421 ArgGlyValValArgArgCysLeuAsnLeuGluGluLysValValLeuLysArgPheCys 440
DB 1261 CGAGCGTGTGCTCGCGCTGCTCAATCTGAGGAAAGATGTGCTGAAAGCGCTTCTGC 1320
QY 441 ArgMetAlaValGluGluValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
DB 1321 GATATGCTGTGAGGAGAGTGTGAATGAAGATCAATGTGATGTGATGATGATGATGATGATG 1380
QY 461 ValGlnGlyLeuGluGluSerGluLeuArgAlaLeuPheHisSmeAsnIleLeuLeuPro 480
DB 1381 GTTCAAGGATCTCGGAGAGTCTGAGCTCCGTCTCTGTTCACATGAACATCTTCTCCA 1440
QY 481 AspSerHisCysGluGluTyrglyThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
DB 1441 GACAGCCTATGTAGAGATCTACACTCTTCCACTCAAGTCCAGGACTTCTGTGCC 1500
QY 501 AlaLeuTyrglyValLeuGluGluGluGluIleGluProAlaLeuCysProLeuTyrglyVal 520
DB 1501 GCTTGTACTACGTGTGAAGGCTGGAATCAAGCAGCTCTCTGCTGTACGTT 1560
QY 521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisSileHisSerLeuTrp 540
DB 1561 GAGAAACAAAGAGTCTCATGAGCTTAAACAGCAGGCTTCCATATCCACTCCGCTTGG 1620
QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
DB 1621 ATGAAGCGTTTCTTGTGGCTCTGTGAGCGAAGACCTAAGAGAGGCTCACTGAGGTCCTG 1680
QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisSerTrpValSerLeuLeu 580
DB 1681 CTGGGCTGTCCCTTCCCTGGGGGTGAACAGAAAGCTTCTGCACTGGGCTCTCTGTGG 1740
QY 581 GlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
DB 1741 GGTAGAGCTTAATGCAACACCCAGAGAGACCTCGACGCTTCCACTGTCTTTC 1800
QY 601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
DB 1801 GAGACTCAAGCAAAAGATTGTGCTGTGCAATTAAACAGCTTCCAAGAAAGTGTGCTT 1860
QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrgly 640
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Db 1861 CCGATTAAACGAACTTGAACTTATGACATCTTCCTTGCCCTCCAGCACTGTCGGTAT 1920
QY LeuArglyValIeArgValIAspValIysGlyIlePheProArgAspGlySerAlaIa 660
Db 1921 TTGGCGAAAATTCGGGTGATGATCAAGGATCTTCCAGAGATGATGATCCGCTAGGCA 1980
QY CysProValIaProLeuTrpMetArgAspIleuIleGluGluGlnTrpGluAsp 680
Db 1981 TGTCCTGTGGTCCCTCTATGATGCGGGAATAGACCTTCATGAGAGACAGTGGGAAGAT 2040
QY PheCysSerMetLeuGlyThrHisIleuArgIleuLeuAspLeuGlySerIle 700
Db 2041 TTCTGCTCCTACGCTTGCGACCCACCACTGCGGAGCTGGACCTGGCGAGCAATC 2100
QY LeuThrGluArgAlaMetIleThrIleuCysAlaIleuArgHisProThrCysIle 720
Db 2101 CTGACAGCGGGCCATAGACCTCTGTGTCAGAGCTGAGGCACTCCACCTGCAAGATA 2160
QY GlnThrIleuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisIleuTrpArgIle 740
Db 2161 CAGACCCGATGTTTAGAAATGACAGATTACCCCTGTGTGACAGCACTCGAGAAATC 2220
QY ValMetAlaAsnArgAsnLeuArgSerIleuAsnIleGlyThrHisIleuIysGluGlu 760
Db 2221 GTCAATGGCCAAACCGTAACCTTAAGATCCCTCAACTGGAGGCACTGACCTGAGAAAG 2280
QY AspValIArgMetAlaCysGluValIleuIysHisProIysCysIleuGluSerIleuArg 780
Db 2281 GATGTAAAGATGGCGTGAAGCCTTAAACACCCAAATGTTTGTAGCTTTTGAGG 2340
QY LeuAspCysCysGlyIleuThrHisAlaCysIleuIysIleSerGlnIleuThrThr 800
Db 2341 CTGAGATCTGTGGATTGATCCCAATGCCCTGTACCTGAAAGATCTCCCAATCTTAAGAC 2400
QY SerProSerIleuIysSerIleuSerIleuAlaGlyAsnIysValIThrAspGlnIysValMet 820
Db 2401 TCCCCAGCCCTGAATCTCTAGGCTGTGGCAGAGAAACAAGTGACAGACAGAGAGTAATG 2460
QY ProIleuSerAspAlaIleuArgValIleuGlnCysAlaIleuGlnIleuValIleuGluAsp 840
Db 2461 CCTCTCAAGTAAAGCTTGAAGTCTCCAGTGGCCCTGCAAGACCTAATCTGAGAGAC 2520
QY CysGlyIleThrAlaThrGlyIleuGlnSerIleuAlaSerAlaIleuValSerAsnArgSer 860
Db 2521 TGTGGCATCAAGCAGCCGGTGGCCAGAGTCTGGCTCAGCCCTGTCAGACACCGGAGC 2580
QY LeuThrHisIleuCysIleuSerAsnAsnSerIleuGlyAsnGluGlyValIAsnIleuCys 880
Db 2581 TTGACACACCTGTGCTATCCAAACAAGCTGGGGAAAGAAAGGTAAATCTACTGTGT 2640
QY ArgSerMetAlaGluProHisCysSerIleuGlnIleuMetIleuAsnGlnCysHisIleu 900
Db 2641 CGATTCATGAGGCTTCCCACTGTAAGTGTGACAGAGGCTGAATCAAGTCCACCTG 2700
QY AspThrAlaGlyCysGlyPheIleuAlaIleuMetGlyAsnSerTrpLeuThrHis 920
Db 2701 GACACGGCTGAGCTGTGTTTCTTGCACTTGCCCTTAAGGTAACTCATGGCTGACGAC 2760
QY LeuSerIleuSerMetAsnProValGluAspAsnGlyValIysIleuIleuCysGluValMet 940
Db 2761 CTGAGCCTTAGACAGAACCTGTGGAGACATGGCGTGAAGCTTCTGTGGAGGTATCAG 2820
QY ArgGluProSerCysHisIleuGlnAspLeuGluIleuValIysCysHisIleuThrAlaAla 960
Db 2821 AGAAGAACCATCTTGTTCATCTCAGAGACCTGAGATTGTGAAGTGCATCTCACCCGCCG 2880
QY CysCysGluSerIleuSerCysValIleSerArgSerArgHisIleuIysSerIleuAspLeu 980
Db 2881 TGCTGTGAGATCTGTCTGTGTATCTCGAGAGACACACCTTAAGAGCTGATCTTC 2940
QY ThrAspAsnAlaIleuGlyAspGlyGlyValAlaAlaIleuCysGluGlyIleuIysGlnIys 1000
Db 2941 ACGGACATGCTCCCTGGGTGACGAGGTGGGTGTCTGTGCGAGGAGCTAGAGCAAAAG 3000

QY AsnSerValIleuThrArgIleuGlyIleuIysAlaCysGlyIleuThrSerAspCysGly 1001
Db 3001 AACAGTGTCTGACGAGACTCGGGTTGAAGGACATGACATGATCTGATGCTGTGAG 3060
QY AlaIleuSerIleuAlaIleuSerCysAsnArgHisIleuThrSerIleuAsnIleuValGlnAsn 1040
Db 3061 GCACCTCTCCCTTGCCCTTCTGCAACCGGACATGACAGAGCTTAACCTGTGTGAGAT 3120
QY AsnPheSerProIysGlyMetIleIysIleuCysSerAlaPheAlaCysProThrSerAsn 1060
Db 3121 AACTCACTCCCAAGAGATATGAGCTGTGTGAGCTTGTGCTGTCCAGTCTAAC 3180
QY LeuGlnIleIleGlyIleuTrpIleTrpIleTrpIleTrpProValGlnIleArgIysIleuGlu 1080
Db 3181 TTACAGATTAATGGCTGTGAAATGAGCATGACCTGTGCAAAATAGAGAGAGTGTGGAG 3240
QY GluValGlnIleuIleuIysProArgValIleIleAspGlySerTrpHisSerPheAspGlu 1100
Db 3241 GAAGTGACGTAATCAAGCCCGAGTCGTAAATGACGAGTATGGCATTTCTTTGATGA 3300
QY AspAspArgHisIleuIleGlyIleuThrPheArgIleuProGlyIleuSerArgAlaTrpProCys 1120
Db 3301 GATGACGACCAAAATGAGACTTACTTCCGCTCCCTGAAAGCCGGCCAGTGCATGT 3360
QY AlaIleuLeuTrpGlyMetAsnProGluGlnIleIysIysArgValSerIleuAlaGlyAsp 1140
Db 1141 GCTTGTCTGTGGGGATTAACCCAGAGCAAGAAAGCTGTGTCTGCTGCTGAGAAC 3420
QY PheIysSerSerThrArgPheAlaIysSerIleuCysIleuAlaThrAlaAsnGlyIleuSer 1160
Db 3421 TTCAAGAGCAGTAACAGATTGCCAAAGTCTCTGTGCTGGCCAGCGCAAAATGATGATCC 3480
QY GlnArgValAspAsnValGluGlnIleSerSerProGlnProMetAlaGlyIleThrGlnHisIleu 1180
Db 3481 CAGAGAGTTGACAAAGTGGACAGAGCTCCCGCAACCAATGAGCGAGGACGAAACA 3540
QY GlnAspIysMetLeuSerValGlyIleSerGlyAlaIleTrpSerGluThrAlaGluIleuGlu 1200
Db 3541 CAAAGTAAATGTTGAGTGTGATATTCGGAAGCTGTGTGAAATGCTGAGCTGCA 3600
QY GlnIleuGlySerAsnSerAlaAspHisAspHisGlyIleMetAlaTrpSerIleuGlyArg 1220
Db 3601 GGGCTGTGATCAACAGTGCATCATGACCAAGGAGTATGGCTGTCTCATAGGAGAG 3660
QY GluIleuSerSerArgGlyIleuCysProThrValIleuMetThrThrAlaValCysProGly 1240
Db 3661 GAGCTGAGCTCGAGGGGCTGTGTGTCCAAGTGTGATGACACACGCGTGTGTCTGTGT 3720
QY HisTrpGluArgIleuGlySerArgGlyIleTrpCysIleuAsnSerAlaAspAspHisSerGly 1260
Db 3721 CACTGGAGCGGCTGGGCTCTAGGGGCTGTGTCTTAAGTGTGATGACACAGCGGT 3780
QY ValSerTrpSerIleuGlyAlaAlaGlyIleuGluIleuValIleSerAsnSerAlaAspAsp 1280
Db 3781 GTGTCTGTGATCACTGGAGCGGCTGGCTGAGGGGCTGTGTCTCAACAGTGTGATGAC 3840
QY HisSerGlyValAlaTrpSerIleuGlyAlaAlaGlyIleuGluIleuValIleSerAsnSer 1300
Db 3841 CACAGCGGTGTGGCTGTGCTACTGGAGCGGCTGGGCTGAGGGGCTGTGTCTCAACAGT 3900
QY AlaAspAspHisSerGlyValIleTrpSerIleuGlyAlaAlaGlyIleuGluIleuValIle 1320
Db 3901 GCTATGACCAAGCGGTGTGTCTGTGTGATCTGGAGGCGGCTGGGCTGAGGGGCTGTGTG 3960
QY SerAsnSerAlaAspAspHisSerGlyValIleSerTrpSerIleuGlyAlaAlaGlyIleuGlu 1340
Db 3961 TCCAACAGTGTGATGACCAAGGCGTGTGTCTGTGTCACTGGAGCGGCTGGGCTGAG 4020
QY GlyIleuValSer 1344
Db 4021 GGGCTGTGTGTCT 4032

RESULT 2

US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US2003002757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Welye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 0734-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
; US-10-066-521-5

Alignment Scores:

Pred. No.:	0	Length:	4035
Score:	1344.00	Matches:	1344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	14	Gaps:	0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrgLysLeuGlnTrpCysLeuTyrgLys 20
DB 1 ATGGAAGAGCAAAATCGCTCACTTTCCAGCTACGGGCTGCATGCTGTCTATACAG 60
QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGlnSer 40
DB 61 CTAGACAAGAGAAATTCAGACATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCG 120
QY 41 ThrThrCysSerLeuIleProGlnPheGlnIleGluLeuLeuLeuLeuLeuLeuLeu 60
DB 121 ACCCAATGCTCTATTCACAGATTGAAATTCAGAAATTCAGAAATTCAGAAATTCG 180
QY 61 LeuLeuHISGluTyrgLysLysSerLeuLysLeuLysLeuLysLeuLysLeuLysLeu 80
DB 181 CTCTTCGATGAGTATTAATGAGCATCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 81 AsnMetAsnLeuAspGlnLeuSerGlnLysLysLysLysLysLysLysLysLysLys 100
DB 241 AACATGAACCTGCAGAACCTCTCGGAGAGGCAAGGATGACATGAAATTCAGAA 300
QY 101 AlaMetGluGlnGluGluLysLysLysLysLysLysLysLysLysLysLysLysLys 120
DB 301 GCTATGGAACAAAGAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 360
QY 121 MetGluGlnGluGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140
DB 361 ATGGAACAAAGAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
QY 141 TrpAspTyrgLysSerHisValMetThrLysPheLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 421 TGGGACTACAGAGTCACTGATGACAAATTCGCTGAGAGAGAGAGAGAGAGAGAGAG 480
QY 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyLysPheAspSer 180
DB 481 TTGTAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 181 AspArgTrpGlyPheArgProArgThrValValLeuHISGlyLysSerGlyLysGlyLys 200
DB 541 GACCGGTGGGGCTTCGCGCTTCGACAGGTGGTCTGACAGGAAGTCAGGAATTCGAGAAA 600
QY 201 SerAlaLeuAlaArgGlyLysLeuCysTrpAlaGlnGlyLysLeuTyrgLysGlnLys 220
DB 601 TCGGCTCTACGCAAGAGATCGTGTGCTGGGCGGAGGTGACCTCTACAGAGATG 660
QY 221 PheSerTyrgLysPhePheLeuProValArgGluMetGlnArgLysLysGlnSerSerVal 240
DB 661 TTCTCTACGCTCTTCTCTCTCCCGTTAGAGATGACGCGAAGAGAGAGAGAGAGAGTC 720
QY 241 ThrGlnPheLysSerArgLysTrpProAspSerGlnAlaProValThrGluLysMetSer 260
DB 721 ACAGAGTTCATCTCCAGAGGATGGCCAGACTCCAGGCTCCGGGAGCAGAGATCATGTGCC 780
QY 261 ArgProGluArgLeuLeuPheLysLysLysLysLysLysLysLysLysLysLysLys 280
DB 781 CGACCAAGAAAGGCTGTGTTCATCATGACGGTTCATGACCTGCTGCTGCTGCTGCTGCT 840
QY 281 AsnAspThrLysLysLysCysLysAspTrpAlaGluLysGlnProPheThrLeuLysArg 300
DB 841 AATGACCAAGAGCTCTGCAAGAGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 SerLeuLeuArgLysValLeuLeuProGlnSerPheLeuLysValThrValArgAspVal 320
DB 901 AGTCTGCTGAGAGAGCTGCTGCTCTCGAGTCTTCTGATCGTCACTGCTGAGAGAGAG 960
QY 321 GlyThrGluLysLeuLysSerGluValLysSerProArgTyrgLysLeuValArgLys 340
DB 961 GGCACAGAGAGAGCTCAAGTCAAGAGTGTGTCTCCCGTTACCTGTAGTTAGAGAGATC 1020
QY 341 SerGlyGluGlnArgLysLysLysLeuLeuGlnArgLysLysGlyLysLysLysLysThr 360
DB 1021 TCCGGGAAACAAAGATTCATCTGCTCTGAGGCGGGATGGTGGAGCATCAGAAAGCA 1080
QY 361 GlnGlyLeuArgAlaLysMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
DB 1081 CAAGGTTGGGTGGATCAGTAAACAGTGAAGTGTCTGACAGCAGTCCAGAGTCCCGGCC 1140
QY 381 ValGlySerLeuLysCysValAlaLeuGlnLeuGlnAspValValGlyLysSerValAla 400
DB 1141 GTGGGCTCTCTCACTCTCGTGGCCCTGACGTGACGAGACGTGTGGGAGAGAGGTGCC 1200
QY 401 ProPheAsnGlnThrLeuThrGlyLeuHISAlaAlaPheValPheHISGlnLeuThrPro 420
DB 1201 CCTTCAACCAAGCTCAAGGCTCAAGGCTGACGCGCTTTGTGTTCTATCAGCTCACCCCT 1260
QY 421 ArgGlyValValArgArgCysLeuAsnLeuGlnGluArgValValLeuLysArgPheCys 440
DB 1261 CGAGGCGTGGTCCGGCGCTGCTCAATCTGAGAGAAAGATGTCCTGAAAGCGCTTGCGC 1320
QY 441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
DB 1321 CGTATGCTGTGGAGGAGGTGTGAATGGAAGTCACTGTGTGATGAGTACGACCTCATG 1380
QY 461 ValGlnGlyLeuGlyLysGlnLeuArgAlaLeuPheHISMetAsnLysLeuLeuPro 480
DB 1381 GTTCAGAGACTCGGGAGGTGAGCTCGTGTGTTTCAATCAAGAACATCTCTCCCA 1440
QY 481 AspSerHisCysGluGluTyrgLysTrpPhePheHISLeuSerLeuGlnAspPheCysAla 500
DB 1441 GACAGCACTGTAGAGAGTACTACACTTCTTCCACTCAGTCTCCAGAGCTTGTGCC 1500
QY 501 AlaLeuTyrgLysValLeuGlnGlyLeuGlnLysGlnProAlaLeuCysProLeuTyrgVal 520
DB 1501 GCTTGTACTACAGTGTAGAGGCTGGAATGAGCAGAGCTCTGCTGCTGCTGCTGCTGCT 1560
QY 521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyLysLysLysLysLysLysLys 540
DB 1561 GAGAAAGCAAGAGTCCATGAGACTTAAACAGGCAAGCTTCCATATCCACTGCTTTGG 1620

QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 1621 ATGAAGCGTTCTTGTTGGCTCGTGAGCGAAGACGTAAAGAGGCGCATGGAGGTTCTTG 1680
QY 561 LeuGlyCysProValProLeuGlyValIlySerGlnIlyLeuLeuHleTTPValSerLeuLeu 580
Db 1681 CTGGGCTGTCTCCCTGGGCTGGGAGGAGGAGGCTTGGCATCTGGCATCTGCTCTGTTGG 1740
QY 581 GlyGlnGlnProAspAlaThrThrProGlyAspThrLeuAspAlaPheHleCysLeuPhe 600
Db 1741 GGTGAGCGAGCTTAATGCAACACCCAGAGACACCTTGAGAGCTTCACTGTTCTTTTC 1800
QY 601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTTPLeu 620
Db 1801 GAGACTCAAGACAAAGAGTTTGTGCTTGGCATTAACAGCTTCCAAAGATGTGGCTT 1860
QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHleCysProTyr 640
Db 1861 CCGATTAAACGAACCTGGAATGATGACATCTTCTGCTGCTCCAGACACTGTCCTGAT 1920
QY 641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660
Db 1921 TTGGGAAAATTCGGGTGAATGTCAAGGAGATCTTCCAAAGATGAGTCGGCTGAGGCA 1980
QY 661 CysProValValProLeuTTPMetArgAspLysThrLeuIleGluGluGluTTPGluAsp 680
Db 1981 TGTCTGTGCTCTCTTAATGATGGGAGTAAAGACCTCATTTAGAGACAGTGGGAAAT 2040
QY 681 PheCysSerMetLeuGlyThrHleProHleAspArgGlnLeuAspLeuGlySerSerIle 700
Db 2041 TTCTGCTCATGCTGTGGCACCACCACCACTGGCGAGCTGAGCTGGGAGCAGCATC 2100
QY 701 LeuThrGluValAspAlaMetLysThrLeuCysValLysLeuArgHleProThrCysLysIle 720
Db 2101 CTGACAGAGCGGCGCATGAAGACCTGTGTGCAGAGCTGAAGCATCCACCTGCAGAGTA 2160
QY 721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHleLeuTTPArgIle 740
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QY 761 AspValArgMetAlaCysGluAlaLeuLysHleProLysCysLeuLeuGlnSerLeuArg 780
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QY 801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnIlyValMet 820
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QY 821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
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QY 841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
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QY 861 LeuThrHleLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCys 880
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QY 881 ArgSerMetAlaGluProHleCysSerLeuGlnArgLeuMetLeuAsnGlnCysHleLeu 900
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Qy 1281 HissergIyValIaIatrpSerIeugIyAlaIaIagIleugIugIyLeuValSerAsnSer 1300
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Qy 1301 AAlaapaphHissergIyValIserTrpSerIeugIyAlaIaIagIyLeugIugIyLeuVal 1320
Db 3901 GCTATGACCAACAGCGGTGTGTCTCGGTCACTGGAGCGGCTGGGCTTCGAGGGGCTTGTG 3960
Qy 1321 SerAsnSerAlaApaphHissergIyValIserTrpSerIeugIyAlaIaIagIyLeugIu 1340
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Qy 1341 G1yLeuValSer 1344
Db 4021 GGGCTGGTGTCT 4032
RESULT 3
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; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: ARVIZU, Chandra
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0842 PCT
; CURRENT APPLICATION NUMBER: US/10/416,642
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: 60/249,407
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3
Alignment Scores:
Pred. No.: 0 Length: 3489
Score: 1006.00 Matches: 1006
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.85% Indels: 0
Gaps: 0
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Qy 118 SerGlnAlaMetGlnGlnGlnGlnValAlaThrAlaAlaGlnThrGlnGlnGlnGlnUle 137
Db 514 TCACAAAGCTATGAAACAAGAGGTGCCACAGACGACGAGACAGAAACAAGAAACAATGGA 573
Qy 138 G1yAspThrTrpAspTrpLysSerHisValMetThrLysPheAlaGlnGlnGlnUleAspVal 157
Db 574 GGTGACACATGGAGCTACAAAGATCAAGTGAACCAATTCCGTGAGAGAGAGAGATGTA 633
Qy 158 ArgArgSerPheGlnGlnGlnThrAlaAlaAspTrpProGlnMetGlnThrLeuAlaGlyAla 177
Db 634 CGTGTGTGTTTGAACCACTGCTGCTGACCTGGCCGGAAATGCAAACTGTGCTGTGCT 693
Qy 178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197
Db 694 TTGATTCAGACCGGTGGGGCTTCGGGCTCGACAGGTGTTCGACGGAAAGTCAGGA 753

Qy 198 TlLeuLysSerAlaLeuAlaArgArgTlLeuLeuGlyStrAlaGlnGlnGlnGlnUleUtr 217
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Qy 218 GlnGlyMetPheSerTrpValPhePheLeuProValArgGlnMetGlnArgLysGln 237
Db 814 CAGGAAATGTTCTTACGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 873
Qy 238 SerSerValThrGlnPheIleSerArgGlnTrpProAspSerGlnAlaProValThrGln 257
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Qy 258 TlMetSerArgProGlnGlnGlnLeuPheIleIleAspGlyPheAspAspLeuGlySer 277
Db 934 ATCATGTCTCCGACCAAGAGCTGTGTTCATCATTAACGGTTCGATGACCTGGGGCTCT 993
Qy 278 ValLeuAsnAspAspThrLysLeuCysAlaAspTrpAlaGlnLysGlnProProPheThr 297
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Qy 398 SerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGln 417
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Qy 418 LeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGlnGlnArgValAlaLeuLys 437
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Qy 438 ArgPheCysArgMetAlaValGlnGlyValTrpAsnArgLysSerValPheAspGlyAsp 457
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Qy 458 AspLeuMetValGlnGlnLysGlnGlnGlnSerGlnLeuAsnArgAlaLeuPheHisMetAsnIle 477
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Qy 478 LeuLeuProAspSerHisCysGlnGlnUtrTrpThrPhePheHisLeuSerLeuGlnAsp 497
Db 1594 CTTTCCCAACAGCCACTGTGAGAGTACTACCTTCTTCCACTCCACTCCAGAC 1653
Qy 498 PheCysAlaAlaLeuUtrTrpValLeuGlnGlnGlnGlnLeuProAlaLeuCysPro 517
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Qy 538 SerLeuTrpMetLysAspPheLeuPheGlyLeuValSerGlnAspValArgArgProLeu 557
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Db      1834 GAGGTCCTGGGCTGTCCCGTCCCTGGGGGGGAGAGCAGAGCTTCTGCACTGGGTC 1893
Qy      578 SerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHis 597
Db      1894 TCTCTGTGGGTGAGCAGACCTTAATGCCACACCCGAGAGACACCTTGAGCGCTTCCAC 1953
Qy      598 CysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGlu 617
Db      1954 TGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCCTTGCGATTAAAGCTTCCAAAGA 2013
Qy      618 ValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHis 637
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Qy      638 CysProCylLeuAlaGlyLysIleArgValAspValLysGlyIlePheProArgAspGlnSer 657
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Qy      658 AlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGln 677
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Qy      678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697
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Qy      698 SerSerIleLeuThrGlnArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThr 717
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Qy      718 CysAlaLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValIleGlnHisLeu 737
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Qy      738 TrpArgIleValIleMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeu 757
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Qy      758 LysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlu 777
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Qy      798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGln 817
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Qy      818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIle 837
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Qy      838 LeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerHisLeuValSer 857
Db      2674 CTGAAGAGATGTGATCAGACAGCCAGGGTGGCCAGATCTGGCTCAGCCCTGCTCAGC 2733
Qy      858 AsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlyIleValAsn 877
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Qy      878 LeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnIleArgLeuMetLeuAsnGln 897
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Db      2854 TGCACCTGAGACAGGGCTGGCTGTGTTTCTTGACATCTGGCTTATGAGGTAACTCAAG 2913
Qy      918 LeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuCys 937

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Db      2914 CTGACGACCTGAGCTTAGCATGAACCTGTGTGAAGCAATGGCGTGAACCTTCTGTGC 2973
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Db      2974 GAGGTATGAGAGAACCATCTTGTATCTCCAGAGCTGGAGTTGTAAAGTATCTC 3033
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Qy      978 LeuAspLeuThrAspAsnAlaLeuGlyAspGlyIleValAlaAlaLeuCysGluGlyLeu 997
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Qy      998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAsp 1017
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Db      3274 GTGCAGATTAATCTTCAAGTCCCAAGAGATGATGAAGCTGTGTGGCTTGTGCTGCC 3333
Qy      1058 ThrSerLeuLeuGlnIleIleGlyLeuThrPheTrpGlnTrpProValGlnIleArgLys 1077
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Qy      1078 LeuLeuGluGluValAlaGlnLeuLeuLysProArgValValIleAspGlySerThrHisSer 1097
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; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAEL
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-1

Alignment Scores:
Pred. No.: 0 Length: 3926
Score: 1006.00 Matches: 1006
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.85% Indels: 0
DB: 15 Gaps: 0

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Qy 238 SerSerValThrGluPheIleSerArgGluTrpProAapSerGlnAlaProValaThrGlu 257
Db 874 AGCAGTGTCAAGAGTTCAATCTCCAGGAGAGTGGCCAGACTCCAGGCTCCGTTGACGAG 933
Qy 258 IleMetSerArgProGluArgLeuLeuPheIleIleAapGlyPheAapAapLeuGlySer 277
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Db 1114 AGAGCGTGGCAGCAGAAAGCTCAAGTCAAGGCTGCTCTCTCTCTCTCTCTCTCTCT 1173
Qy 338 ArgGlyIleSerGlyGluGluAapGlyIleHisLeuLeuGluArgGlyIleGluGluHis 357
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Db 1294 GTGCCCGCGTGGCTCTCATCTGCGTGGCCCTGCAGCTGACAGAGTGTGGGGAG 1353
Qy 398 SerValaIaProPheAaenGluInThrLeuThrGlyLeuHisAlaAapPheValaGlu 417
Db 1354 AGCGTCGCCCCCTTCACCAACCAAGCTCAAGGCTGCAGCGCTTTGTGTTCATCAG 1413
Qy 418 LeuThrProAapArgGlyValaIaArgArgCyLeuAaenLeuGluGluArgValaIleuLys 437
Db 1414 CTCACCCCTCAGAGCGGTGCTCGCGCTGTCTCAATCTGAGAGAAAGTGTCTCTGAG 1473
Qy 438 ArgPheCyAapGmeAlaValaGluGlyValaTrpAaapTrpSerValaPheAapGlyAap 457
Db 1474 CGCTTCGCGGTAGCGTGTGAGAGGAGTGTGAATAGAAAGTCAAGTCTTTGACGATAC 1533
Qy 458 AapLeuMetValaGlnGlyLeuGlyGluSerGluLeuAapAlaLeuPheHisMetAapIle 477
Db 1534 GACCTCATGTTCACAGGACTCGGGAGTGTGAGCTCCGTGCTGTGTTCAATGAACTAC 1593

Qy 478 LeuLeuProAapSerHisCySegGluGluTrpTrpThrPhePheHisLeuSerLeuGluAap 497
Db 1594 CTCTCCACAGACAGCTGAGAGAGTACTACACTTCTCTCCACTCAGCTCCAGAGAC 1653
Qy 498 PheCyAaIaIaLeuTrpTrpValaIleuGluGluLysLeuGluIleGluProAlaLeuCyAPro 517
Db 1654 TTTCTGCGCGCTTGTACTAGTGTAGAGGCTGGAAATCGAGCAAGCTCTGTGCCCT 1713
Qy 518 LeuTrpValaGluLysThrLysAapSerMetGluLeuLysGlnaIaGlyPheHisIleHis 537
Db 1714 CTGTACCTGAGAGAGACAAAGGTCATGAGCTTAAACAGAGGCTTCCATATCCAC 1773
Qy 538 SerLeuTrpMetLysAapPheLeuPheGlyLeuValaSerGluAapValaArgArgProLeu 557
Db 1774 TCGCTTGAATGAAGCGTTTCTTGTGGCTCGTGAAGCAGACGTAAAGAGGCGCACTG 1833
Qy 558 GlnValaLeuLeuGlyCyProValaProLeuGlyValaLysGlnLysLeuHisIleTrpVal 577
Db 1834 GAGGTCTGTGGGCTGTCTCCGTCTCCCTGGGGGTGAAGAGCAAGATTTGTGCACTGGAGTC 1893
Qy 578 SerLeuLeuGlyGlnGluInProAaenAlaThrThrProGlyAapThrLeuAapAlaPheHis 597
Db 1894 TCTCTGTGGGTCAAGAGCTTAATGCCACACCCAGAGACACCTTGACGCTTCCAC 1953
Qy 598 CyAaenPheGluThrGlnAapLysGluPheValaArgLeuAlaLeuAaenSerPheGlnGlu 617
Db 1954 TGTCTTTGCAAGCTCAAGACAAAGATTTGTTGCTGGCTTGAACATTAACGCTTCCAGAA 2013
Qy 618 ValTrpLeuProIleAaenGlnAaenLeuAapLeuIleIleAapSerPheCyAaenGluHis 637
Db 2014 GTGTGGCTTCGATTAACAGAACTGGAATCTGTATACATTTCTCTGTGCTTCACAGAC 2073
Qy 638 CyAProTrpLeuAapLysIleArgValaAapValaLysGlyIlePheProAapArgGlySer 657
Db 2074 TGTCCGATTTGGCGGAAATTCGGGTGATGTCAAGAGATTTCCAAAGAGAGATGCC 2133
Qy 658 AlaGluAlaCyProValaProLeuTrpMetArgAapLysThrLeuIleGluGluGln 677
Db 2134 GCTGAGGCAATGCTCGTGTGCTCTCTATGAGTGGGATGAAGACCTTCATTAAGAGACAG 2193
Qy 678 TrpGluAapPheCyAapSerMetLeuGlyThrHisAroHisLeuAapGluAaAapLeuGly 697
Db 2194 TGGGAATTTCTGCTCAGCTGAGCTTGGACCCACCACTGCGGAGCTGAGCTGAGCTG 2253
Qy 698 SerSerIleLeuThrGluAapAlaMetLysThrLeuCyAaIaLysLeuAaHisProThr 717
Db 2254 AGCAGCATCTCGACAGACCGGGCCATGAACCTGTGTGCCAAGCTGAGGCACTCCAC 2313
Qy 718 CyAaLysIleGluInThrLeuMetPheArgAaAaIaGlnIleThrProGlyValaGlnHisLeu 737
Db 2314 TGCAGATTAACAGACCTGATGTTAAGAAATGCACAGATTAACCTCGGTGTGACAGACTC 2373
Qy 738 TrpArgIleValaMetAlaAaenArgAaenLeuArgSerLeuAaenLeuGlyThrHisLeu 757
Db 2374 TGGGAATCGTCAGAGGCAACCGTAACTTAAGATCCCTCAACTTGGAGGACCACTGCTG 2433
Qy 758 LysGluGluAapValaArgGmeAlaCySegLysAlaLeuLysHisAapProLysCyAaenLeuGlu 777
Db 2434 AAGGAAGAGTGAAGATGAGCTGTGAAGCTTAAACACCCAAATGTTTGTGTGAG 2493
Qy 778 SerLeuArgLeuAapCyAaGlyLeuThrHisAlaCyTrpLeuLysIleSerGlnIle 797
Db 2494 TCTTTAGGGCTGAGATTCGTGATTAACCAATCCGTTAACTGAAGATCTCCAAATC 2553
Qy 798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAaenLysValaThrAapGln 817
Db 2554 CTTAACGACTCCCACTGAATCTGAGCTTGCAGGAAACAAGTGAAGAGACAG 2613
Qy 818 GlnValaMetProLeuSerAapAlaLeuArgValaSerGlnCyAaIaLeuGlnLysLeuIle 837
Db 2614 GAGGAATATGCTCTCAAGTGAATGCTTGAAGATTCACAGTGTGCGCTTCAGAAAGCTGATA 2673

QY 838 LeuGluAapCySgLyIleThrAlaThrGlyCySgInSerLeuAlaSerAlaLeuValSer 857
Db 2674 CTGAGAGACTGTGGCATACAGCCAGCGGTTGCCAGAGTCTGGCCCTCAGCCCTGTGTACAGC 2733
QY 858 AsnArgSerLeuThrHisLeuCySgLeuSerAsnAsnSerLeuGlyValAsnGlyValAsn 877
Db 2734 AACCGAGCTTGAACACCTGTGCTTATCCAAACACCTGGGGAACGAAAGTGTAAAT 2793
QY 878 LeuLeuCySgSerMetArgLeuProHisCySgSerLeuGlnArgLeuMetLeuAsnGln 897
Db 2794 CTACTGTCTCATCATAGAGGCTTCCCACTGTATCTGCAAGAGCTGATGCTGAATCAG 2853
QY 898 CySHisLeuAapThrAlaGlyCySgLyPheLeuAlaLeuAlaMetGlyValAsnSerTrp 917
Db 2854 TGCCACCTGACACAGGCTGGCTGTGGTTTCTTGCACCTTGCGCTTATGGGTAACTCATAG 2913
QY 918 LeuThrHisLeuSerLeuSerMetAsnProValGluAapAsnGlyValLysLeuLeuCyS 937
Db 2914 CTGACGCACTGAGGCTTGAACATGAACCTGTGGAAGCAATGGGCTGAAGCTTCTGTGC 2973
QY 938 GluValMetArgGluProSerCySHisLeuGlnAapLeuGluLeuValLysCySHisLeu 957
Db 2974 GAGGTCAATGAGAACCATCTTGTATCTCCAGACCTGAGATTGTAAAGTGTATCTC 3033
QY 958 ThrAlaAlaCySgCySgLeuSerCySValLysSerArgSerArgHisLeuLysSer 977
Db 3034 ACCGCGGCTGTCTGTGAAGTCTGTCTGTGTATCTGAGGAGCAACCTGAAAGC 3093
QY 978 LeuAapLeuThrAapAsnAlaLeuGlyAapGlyValAlaAlaLeuCySgGlyLeu 997
Db 3094 CTGATCTCAAGCAATGCCCTGGGTGACGATGGGGTGGCTGCTGCGAGGAGACTG 3153
QY 998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCySgGlyLeuThrSerAsp 1017
Db 3154 AAGCAAAAGAACAGTGTCTGACGACTCGGTTGAAGGCAATGGAGCTGATCTTAT 3213
QY 1018 CySgCySgAlaLeuSerLeuAlaLeuSerCySAsnArgHisLeuThrSerLeuAsnLeu 1037
Db 3214 TGCTGTAGGCACTCTCTTGGCCCTTCTGTGCAACCGGCATCTGACCAAGTAAACTG 3273
QY 1038 ValGlnAsnAsnPheSerProLysGlyMetCysLeuCySgSerAlaPheAlaCySgPro 1057
Db 3274 GTGAGATATACCTTCAATCCCAAGAGATGATGAAGCTGTGTCCGCCCTGTGCC 3333
QY 1058 ThrSerAsnLeuGlnLysLeuGlyLeuThrLysTrpGlnTrpProValGlnLysArgLys 1077
Db 3334 ACGTCTAACTTACAGATTAATGGCTGTGAAATGGCACTGCCGTCAATTAAGAGAG 3393
QY 1078 LeuLeuGluGluValGlnLeuLeuLysProArgValValLysGlySerTrpHisSer 1097
Db 3394 CTGCTGAGAGAAAGTGCAGCTCAAGCCCGAGTGTAAATTGAAGGTAGTTGGCATTTCT 3453
QY 1098 PheAapGluAapAspArg 1103
Db 3454 TTTGATGAAGATGACCGG 3471

RESULT 5
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAEL
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 3
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-3
Alignment Scores:
Pred. No.: 0 Length: 3830
Score: 988.00 Matches: 988
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.51% Indels: 0
DB: 15 Gaps: 0
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QY 116 GluLysSerGlnAlaMetGluGlnGluGlyValAlaThrAlaAlaGluThrGluGluGlnGly 135
Db 451 GAATTTTCAAGAGCTATGTGAACAAAGAGCTGCCACAGCAGACAGACAGAAAGCAAGCA 510
QY 136 HisGlyGlyAapThrTrpAspTrpLysSerHisValMetThrLysPheAlaGluGluGlu 155
Db 511 CATGAGGTGACACATGGGACTTACAGAGTCACTGATGACCAATTCCTGAGAGAGAG 570
QY 156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
Db 571 GATGTACTCGTATGTTTGAATAACATGCTGCTGACTGGCCGGAATCCAAACGTTGGCT 630
QY 176 GluAlaPheAapSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLys 195
Db 631 GATGCTTTGATTGATCAGACCGGTGGGGCTTCCGGCTCCGACAGGTGTCTGCACGGAAG 690
QY 196 SerGlyLysGlyLysSerAlaLeuAlaArgArgGlyLeuLeuCySgTrpAlaGlnGly 215
Db 691 TCAGGAATTTGGAAATCGCTCTTACCGCAAGAGATCGTGTGTGGGCGCAAGTGA 750
QY 216 LeuTrpGlnGlyMetPheSerTrpValPhePheLeuProValArgGluMetGlnArgLys 235
Db 751 CTATCAAGGGAATGTTCTCTTACGTCTTCTCTCCCGTTAAGAGATCAAGCGGAG 810
QY 236 LysGluSerSerValThrGluPheLysSerArgGluTrpProAapSerGlnAlaProVal 255
Db 811 AAGAGAGCAATGTCCACAGATTCATCTCCAGGAGTGGCCAGACTCCCAAGCTCCGGT 870
QY 256 ThrGluMetSerArgProGluArgLeuLeuPheLysLeuAspGlyPheAspAspLeu 275
Db 871 ACGAGATCATGTCCCAACGAAGGCTGTGTTCATCATATGACGTTTGATGACTG 930
QY 276 GlySerValLeuAsnAsnAspThrLysLeuCySgLysAspTrpAlaGluLysGlnProPro 295
Db 931 GGTCTGTCTTCAACATGACAAAGCTTGCAAAGACTGGCTGAGAAAGCAAGCTCCG 990
QY 991 PheThrLeuLysArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuLysVal 315
Db 991 TTCACTCATATACCACTGCTGAGAAAGTCTGTCTCCCTGAGTCTTCTGATCGTCTC 1050
QY 316 ThrValArgAapValGlyThrGluLysLeuLysSerGluValValLysSerProArgTrpLeu 335
Db 1051 ACCGTCAAGACGTTGGGCAAGAGACTCAAGTCAAGAGTGTGTCTCCCGTTTACTG 1110
QY 336 LeuValArgGlyLysSerGlyGluGlnArgGlnLysHisLeuLeuGluValArgGlyVal 355
Db 1111 TTAGTTAAGGAATCTCCGGGAAACAAAGATCCATCTTCTCTTGAACCGGGAATGGT 1170
QY 356 GluHisGlnLysTrpGlnGlyLeuArgAlaLysMetAsnAsnArgLysLeuLeuAapGln 375
Db 1171 GAGCATCAGAAACAAAGGTTCCGTGCATATGAACAACCGTGAAGCTCTGCACAG 1230
QY 376 CySgGlnValProAlaValGlySerLeuLysValAlaLeuGlnLeuGlnAapValVal 395
Db 1231 TGCCAGGTCCCGGCTGTGTCTCATCTGCTGTGCCCTGCAGCTGCAGAGGTGGTG 1290
QY 396 GlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415

Db 1291 GGGAGACGTCGCCCCCTTTCAACCAACGCTCACAGGCTGACGCGCTTTGTGTTT 1350
Qy 416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluValArgVal 435
Db 1351 CATGAGCTCACCCCTCGAGGCGTGCGTCCGGCGCTGTCAATCTGGAGAAAGTTGTC 1410
Qy 436 LeuLysArgPheCysArgMetAlaValGluGlyValTyrAsnArgLysSerValPheAsp 455
Db 1411 CTGAAGCGCTTCTCGCGTATGCGTGTGAGGAGGTGTGAAATAGGAATCGTGTTCAC 1470
Qy 456 GlyAspAspLeuMetValGlnGlyLeuGlyGlnSerGlnLeuArgAlaLeuPheHisMet 475
Db 1471 GGTGACGACTCATGCTTCAAGAGACTCGGAGAGTCTAGCTCCGTGCTCTGTTCACATG 1530
Qy 476 AsnIleLeuLeuProAspSerHisCysGlnGlyTyrTyrThrPhePheHisLeuSerLeu 495
Db 1531 AACATCTCTTCCACAGACAGCACGTGAGAGATCTACACTTCTTCACTCACTGATTC 1590
Qy 496 GlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluValIleGlnProAlaLeu 515
Db 1591 CAGACCTTCTGCGCGCTGTACTACGTGTAGAGGCGCTGGAAATCGAGCCAGCTCTC 1650
Qy 516 CysProLeuTyrValGluLysThrLysArgSerMetGlnLeuLysGlnAlaGlyPheHis 535
Db 1651 TGCCCTCTGTACGTTGAGAAACAAAGAGTCCATGAGCTTAAACAGGCGATTCAT 1710
Qy 536 IleHisSerLeuThrMetLysArgPheLeuPheGlyLeuValSerGlnAspValArgArg 555
Db 1711 ATCCACTGCTTGGATGAAAGCTTTCTTTTGGCGCTGTAGAGCAAGTAAAGAGG 1770
Qy 556 ProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuHis 575
Db 1771 CCATCGAGGAGTCTGCTGGGCTGTCCCGTCCCTGGGGGTGAAGCAAACTTCTGAC 1830
Qy 576 TrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAla 595
Db 1831 TGGGCTCTCTGTGTTGGTCAAGACGCTTAATGCCACACCTCAAGAGACCTTGAGCCC 1890
Qy 596 PheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPhe 615
Db 1891 TTCCACTGCTTTTGGAGACTCAAGACAAAGATTTGTGCTTGGCACTTAAACGCTTC 1950
Qy 616 GlnGluValTyrPheProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeu 635
Db 1951 CAAGAAGTGTGCTTCCGATTAAACAGAACTTGACCTGATGACATCTTCTGCTC 2010
Qy 636 GlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAsp 655
Db 2011 CAGCACTGTCGATTGCGGAAAAATTCGGGTGATGTCAAAGGATCTTCCAAAGAT 2070
Qy 656 GlnSerAlaGluAlaCysProValValProLeuThrMetArgAspLysThrLeuIleGlu 675
Db 2071 GAGTCCGCTGAGGAGATGCTGTGTCTCTATGAGAGCGGAGTAAACCTCAATTGAG 2130
Qy 676 GlnGlnTyrGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAsp 695
Db 2131 GAGAGAGTGGAAAGATTTCTGCTCCATGCTTGCAACCCACCACTGCGCAGCTGAC 2190
Qy 696 LeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHis 715
Db 2191 CTGGGACGACGATCTGACAGAGGCGGCATGAAAGCCGTGTGCGCAACCTGAGGAT 2250
Qy 716 ProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735
Db 2251 CCCACCTGCAAGATACAGAACCTGATGTTTAGAAATGACAGATTACCCCTGGTGTGAG 2310
Qy 736 HisLeuTyrArgGlyValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyThr 755
Db 2311 CACCTCTGAGAAATGTCATGCGCAACCGTAACTTAAGATCCCTCAACTTGGAGGCGACC 2370
Qy 756 HisLeuLysGlnGluAspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeu 775

Db 2371 CACCTGAAGAAAGAGATGTAAAGATGCGGTGTAAGCCTTAAACCCAAATGTTTG 2430
Qy 776 LeuGlnSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSer 795
Db 2431 TTGAGTCTTGAAGGCTGATTTGCTGTGATTTGACCAATGCTGTACTGTAATGATCC 2490
Qy 796 GlnIleLeuThrHisProSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThr 815
Db 2491 CAAAATCTTACGACCTCCCCAGCCTGAATACTGTGAGCCCTGGAGAAACAAAGTAC 2550
Qy 816 AspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLys 835
Db 2551 GACCAAGGAGATTAATGCTCTCAATGATGCTCTTGAAGATCTTCCAGTGCCTTCAGAG 2610
Qy 836 LeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeu 855
Db 2611 CTGATTACTGAGAGACTGTGGCATACAGCCACGCGGTTGCCAGATCTGCGCTCAGCCCTC 2670
Qy 856 ValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGly 875
Db 2671 GTCAGCAACCGAGACTTGACACACTGTGCTTATCCAAACACCTGGGGAAAGAGT 2730
Qy 876 ValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeu 895
Db 2731 GTAAATCTACTGTGTCATCATGAGGCTTCCCACTGTAGTCTGCAGAGGCTGATGCTG 2790
Qy 896 AsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsn 915
Db 2791 AATCAGTGCACCTGACACCGCTGCGTGTGTTTCTTGGCACTTGGCGCTTATGGGTAA 2850
Qy 916 SerThrLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeu 935
Db 2851 TCATGGCTGAGGACCTGAGCCTTAGCATGAACCTGTGGAAACAAATGGGTAAAGCTT 2910
Qy 936 LeuCysGlnValMetArgGlnProSerCysHisLeuGlnAspLeuGlnLeuValLysCys 955
Db 2911 CTGTGCAAGGTCATGAGAGAACATCTTTGTCACTTCCAGACCTGAGATTGTAAAGGT 2970
Qy 956 HisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeu 975
Db 2971 CATCTCACCGCGCGTGTGAGAGTCTGTCTGTGTGATCTCGAGGAGACACACTG 3030
Qy 976 LysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGln 995
Db 3031 AAGAGCCTGGAATTCACAGGACAAATGCCGTGGTACGCTGGGCTGTGCACTGTGCGAG 3090
Qy 996 GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThr 1015
Db 3091 GGACTGAAGCAAAAGAACAGTGTCTGACAGAGCTCGGGTTGAAGCATGTGACTGACT 3150
Qy 1016 SerAspCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeu 1035
Db 3151 TGTGATTTGTGTGAGGACCTCTCTTGCGCTTCTCGCAACCGGCACTGACAGTCTA 3210
Qy 1036 AsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAla 1055
Db 3211 AACCTGTGTGCAATTAATTCAGTCCAAAGAGATGATGAAGCTGTGTGGCTTGGCC 3270
Qy 1056 CysProThrSerAsnLeuGlnIleIleGlyLeuThrTyrTyrPheGlnTyrProValGlnIle 1075
Db 3271 TGTCCACGTCCTAATCTTAACATTAATTTGGGCTGTGGAAATGGCATCCCTGTGCAATA 3330
Qy 1076 ArgLysLeuLeuGlnGluValGlnLeuLeuLysProArgValValIleAspGlySerTyr 1095
Db 3331 AGAAAGCTGTGAGGAAAGTGCAGCTACTCAAGCCCGAGTCGTAATTGAGCGTATGG 3390
Qy 1096 HisSerPheAspGluAspAspArg 1103
Db 3391 CATCTTTGATGAAGATGACCGG 3414

RESULT 6
US-10-092-900A-347
; Sequence 347, Application US/10092900A

Publication No. US20040043382A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li, Li
APPLICANT: Zernusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Gorman, Linda
APPLICANT: Miller, Charles E.
APPLICANT: Kerkuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gangoli, Beha A.
APPLICANT: Verne, Corine A.M.
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Tchernyev, Velizar T.
APPLICANT: Fernandes, Elma R.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Gerlach, Valerie
APPLICANT: Liu, Yi
APPLICANT: Anderson, David W.
APPLICANT: Spaderma, Steven K.
APPLICANT: Carterton, Elina
APPLICANT: Leite, Mario W.
APPLICANT: Zhong, Haihong
APPLICANT: Alsbrook, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine B.
TITLE OR INVENTION: No. US20040043382A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-290C
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/283,675
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: USN 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: USN 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/274,191
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USN 60/325,681
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: USN 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USN 60/279,995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USN 60/294,899
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: USN 60/287,424
PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
SEQ ID NO 347
LENGTH: 3226
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (69)..(3168)
US-10-092-900A-347

Alignment Scores:
Pred. No.: 0
Score: 968.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%

Length: 3226
Matches: 968
Conservative: 0
Mismatch: 0

Query Match: 72.02% Indels: 0
DB: 17 Gaps: 0
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DB 249 CATGAGGTGACACATGCGACTACAGAGTCCAGTGAACCAATTCGTGAGGAGAG 308
QY 156 AspValArgSerPheGluAsnThrAlaAspTrpProGluMetGlnThrLeuAla 175
DB 309 GATGACGTCGTAGTTTGAAACACCTGCTCTGACGCGGAATCCAACTGGCT 368
QY 176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgTrpValLeuHiseGlylys 195
DB 369 GGTCTTTTGATTCAGACCGGTGGGCTCCGGCTCCGACGCTGTCTTCACGGAAG 428
QY 196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCystrpAlaGlnGly 215
DB 429 TCAGGAATGGGAATCGCTCTAGCCAGAGATCGTGTGCTGGCGCCAGAGTGA 488
QY 216 LeuTrpGlnGlyMetPheSerTrpValPhePheLeuProValArgGluMetGlnArglys 235
DB 489 CTACACAGGGAATGTTCTCTACGCTTCTCTCCCTCCGTTAGAGATGACGAGAG 548
QY 236 LysGluSerSerValThrGluPheIleSerArgLutTrpProAspSerGlnAlaProVal 255
DB 549 AAGAGACATGTCACAGAGTTCATCTCCAGGAGTGGCCAGACTCCACGGCTCCGGT 608
QY 256 ThrGluIleMetSerArgProGluArgLeuPheIleIleAspGlyPheAspAspLeu 275
DB 609 ACGGAGATCATGTCCGACCAAGAGGCTGTTCATCATTTAGCGGTTGATGACCTG 668
QY 276 GlySerValLeuAsnAspThrLysLeuCystrpAspTrpAlaGluLysGlnProPro 295
DB 669 GGTCTGTCTTCAACATGACACAAAGCTGTGCAAGCTGGCTGAGAACACAGCTCCG 728
QY 296 PheThrLeuIleAspSerLeuArgLysValLeuLeuPProGluSerPheLeuIleVal 315
DB 729 TTCACTTCATACGACGCTCTCTAGAGAGTCTGTCTCTGAGTCTTCTCATGCTC 788
QY 316 ThrValArgAspValGlyThrGluLysLeuLysSerGluValIleSerProArgTrpLeu 335
DB 789 ACCGTCAGAGACGAGGAGACAGAGAGTCAAGTCAAGGTCGAGTCTCCCGTTACCTG 848
QY 336 LeuValArgGlyIleSerGlyGluGlnArgIleHiseLeuLeuGlnArgGlyIleGly 355
DB 849 TTAGTTAGAGGAATCTCCGCGGAACAAAGATCCACTTGTGAGCGCGGATTCGT 908
QY 356 GluHiseGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuAspGln 375
DB 909 GAGCATTCAGAGACCAAGGTTGCTGTCATGACCAACCGTGAAGTCTCGACAG 968
QY 376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
DB 969 TGCAGAGTCCCGCGTGGCTCTCATCTGCGTGGCCCTCGACGCTCAGAGAGTGGTG 1028
QY 396 GlyLysSerValAlaProPheAsnGlnThrLeuThrGlyLeuHiseAlaIlePheValPhe 415
DB 1029 GGGGAGAGCGTCCCTCTCAACCAACGCTCACAGGCTCGACGCGCTTGTGTGT 1088
QY 416 HiseGlnLeuThrProArgGlyValValArgArgCysLeuLeuGlnGluArgValVal 435
DB 1089 CATCAGCTCACCTTCAGAGGCTGTCGCGGCTGTCTCAATTCGAGAAAGTTGTC 1148
QY 436 LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAsp 455
DB 1149 CTGAAGCGCTTCTCCGTATGCTGTGAGGAGATGTGGAATAGAGATCATGTTCAC 1208
QY 456 GlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHiseMet 475
DB 1209 GGTGACACATCATGTTCAGAGACTCGGAGAGTGTGAGCTCCGTGCTGTTCACATG 1268

Qy 476 Asn1IleuLeuProAspSerHisCyseGluGluTyrTyrThrPhePheHisIleuSerIleu 495
Db 1269 AAGATCTCTTCCAGACAGACAGCTGAGGAGTACTACACCTTCTTCCACTCAGTCTTC 1328
Qy 496 GlnAspPheCySAIaIaLeuTyrTyrValIleuGluGluIleGluProAlaIleu 515
Db 1329 CAGGACTTCTGCGGCTTGTACTACGTGTAAAGGGCCCTGAAATGAGCCAGCTCTC 1388
Qy 516 CysProLeuTyrValGluIysThrIysArgSerMetGluLeuIysGlnIaGlyPheHis 535
Db 1389 TGCCCTCTGTAGCTTGAAGAAGCAAGAGTCCATGAGGCTTAAACAGAGGAGCTTCAT 1448
Qy 536 IleHisSerLeuTyrMetIysArgPheLeuPheGluLeuValSerGluAspValArgArg 555
Db 1449 ATCCACTCGCTTGGATGATACAGCTTCTGTGGCCCTCGAGGAGGAAGTAAAGAGG 1508
Qy 556 ProLeuGluValIleuLeuGluIysProValIleuLeuGluValIysGlnIysLeuHis 575
Db 1509 CCACCTGAGAGTCTGCTGGCTGTGCTCCGTCCCTGGGGGTGAAGCAGAGCTTCTGCAC 1568
Qy 576 TrpValSerLeuLeuGluIysGlnIleProAspAlaThrThrProGlyAspThrLeuAspAla 595
Db 1569 TGGGCTCTCTGTTGGGTCAAGACGCTTAATGCCAACCCAGAGAGACCCCTGGAGGCC 1628
Qy 596 PheHisCySAleuPheGluThrGlnAspIysGluPheValArgLeuAlaLeuAsnSerPhe 615
Db 1629 TTCCACTGTCTTTCGAGACTCAAGACAAAGAGTTTTCCTTGGCTTAAACAGCTTC 1688
Qy 616 GlnGluValIleuProIleAsnGlnAsnIleuAsnIleuIleAsnSerPheCySAleu 635
Db 1689 CAAGAAGGTGGCTTCGATTAAACAGAACCTGAGCTTGAATGACTTCTTCTGCTCC 1748
Qy 636 GlnHisCySAProTyrLeuArgIysIleArgValAspValIysGlyIlePheProArgAsp 655
Db 1749 CAGCACTGTCCGTATTGGGAAATTCGGGTGATGTCAAAGGATTTCCAAAGAGAT 1808
Qy 656 GluSerAlaGluAlaCySAProValIleProLeuTyrMetArgAspIysThrLeuIleGlu 675
Db 1809 GAGTCCGCTGAGGAGATGCTGTGTCTCTATGATGCGGAGTAAACCTCCTCATTTGAG 1868
Qy 676 GluGlnTyrGluAspPheCysSerMetLeuGluIysThrHisProHisIleuArgGluLeuAsp 695
Db 1869 GAGCAGTGGGAAGATTCTGTCCATGCTTGACCCACCCACCTGCGGAGCTGAGC 1928
Qy 696 LeuGlySerSerIleLeuThrGluArgAlaMetIysThrLeuCySAAlaIysLeuArgHis 715
Db 1929 CTGGGACGACACATCTTGAAGAGGGCCATGAAGACCTGTGTGCCAATCAGATGAT 1988
Qy 716 ProThrCysIysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735
Db 1989 CCCACCTGCAGATACAGACCTCATGTTTGAATAATGACAGATTACCCCTGTGTGAG 2048
Qy 736 HisLeuTyrArgIleValMetAlaAsnArgAsnIleuArgSerIleuAsnIleuGlyIysThr 755
Db 2049 CACCTTGGAAATGTCATGAGCCAGACCGTAACTCAATCTTGAAGGAGCC 2108
Qy 756 HisLeuIysGluGluAspValArgMetAlaCyseGluAlaLeuIysHisProIysCySAleu 775
Db 2109 CACCTGAAGAGAGATGTAAGATGCGCTGTGAAGCTTAAACACCCAAATGTTTG 2168
Qy 776 LeuGluSerLeuArgLeuAspCyseGlyLeuThrHisAlaCyseTyrLeuIysIleSer 795
Db 2169 TTGAGAGTCTTGAAGGCTGATTGCTGTGATTGAACCCATGCTGTACTGAAGATCTCC 2228
Qy 796 GlnIleLeuThrThrSerProSerIleuIysSerLeuSerIleuAlaGlyAsnIysValThr 815
Db 2229 CAAATCTTACGACTCCCAAGCTTGAATCTGTGAACCTGCGAGGAAGAGTGA 2288
Qy 816 AspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCySAIleuGlnIys 835
Db 2289 GACCAAGGAGATTAAGCTCTCAGTGAATGCTTTGAGAGTCTCCAGTGGCCCTGCAAG 2348
Qy 836 LeuIleLeuGluAspCyseGlyIleThrAlaThrGlyCyseGlnSerLeuAlaSerAlaLeu 855

Db 2349 CTGATCTGAGAGACTGTGGCATCAAGCAAGGATTTGCCAGATCTGGCTCAGCCCTC 2408
Qy 856 ValSerAsnArgSerLeuThrHisIleuCySAleuSerAsnAsnSerIleuGlyAsnGluIys 875
Db 2409 GTCAAGCAACCGAGCTTGAACACACTGTGCTTATCCAAACAAGCTCGGGAAAGAGT 2468
Qy 876 ValAsnLeuLeuCyArgSerMetArgLeuProHisCySAleuGlnArgLeuMetIleu 895
Db 2469 GTAATCTACTGTGTCCATCCATGAGCTTCCCACTGTGTGTGCAAGAGCTGATGCTG 2528
Qy 896 AsnGlnCySAIleuAspThrAlaGlyCyseGlyPheLeuAlaLeuMetGlyAsn 915
Db 2529 AATCAGTCCACCTGAGACAGCGCTGGTGTGTTTCTTGCATCTGGCTTAAAGTAAAC 2588
Qy 916 SerTrpLeuThrHisIleuSerIleuSerMetAsnProValGluAspAsnGlyValIysLeu 935
Db 2589 TCATGGCTGAGACGACCTGAGCTTAAAGTAAACCTTGGAAAGCAATGGGTAACTT 2648
Qy 936 LeuCyseGluValMetArgGluProSerCySAIleuGlnAspLeuGluLeuValIysCyse 955
Db 2649 CTGTGCGAGGTCAATGAGAGAACCATTTGTTCATCTCCAGAGACCTGAGTTGTAAAGTGT 2708
Qy 956 HisLeuThrAlaIaCyseCyseGluSerIleuSerCySAIleuSerArgHisIleu 975
Db 2709 CATCTCACCGCGGTCTGTGAGAGTCTGTCTGTGTGATCTTGAAGAGAGACACCTG 2768
Qy 976 IysSerIleuAspLeuThrAspAsnAlaLeuGlyAspGlyValAlaIaLeuCyseGlu 995
Db 2769 AAGAGCTTGATCTCACAGACATATGCTTGGGTACAGGTGGGTGCTGCACTTGGAG 2828
Qy 996 GlyLeuIysGlnIysAsnSerValIleuThrArgLeuGluIleuIysAlaCyseGlyLeuThr 1015
Db 2829 GACTGAAGCAAAAGAACAGTGTCTGACAGACTTCGGGTGAAGGCAATGGAGCTGACT 2888
Qy 1016 SerAspCyseGluValaLeuSerIleuAlaLeuSerCySAAsnArgHisIleuThrSerLeu 1035
Db 2889 TCTGATTGCTGTGAGGACTCTCTTGGCCCTTTCGCAACCGGACATCTGAACAGTCTA 2948
Qy 1036 AsnLeuValGlnAsnAsnPheSerProIysGlyMetMetIysLeuCyseSerAlaPheAla 1055
Db 2949 AACCTGTGCAGATTAATCTTCAATGCCAAAGATGATGAAGCTGTGGCTTTGCC 3008
Qy 1056 CysProThrSerAsnLeuGlnIleIleGlyLeuTyrIysTrpGlnTyrProValGlnIle 1075
Db 3009 TGTCCACAGTCTAATTAAGATTAATGGGCTGTGAATGGAGCTACCTGTGCATAATA 3068
Qy 1076 ArgIysLeuLeuGluGluValGlnIleuLeuIysProArgValValIleAspGlySerTrp 1095
Db 3069 AGGAAGCTGTGGAGGAAGTCAAGTCTCAAGCCCGAGTCTGAATTTGAACGGTATTTGG 3128
Qy 1096 HisSerPheAspGluAspArg 1103
Db 3129 CATTTTGTATGAAGATGACCGG 3152

RESULT 7
US-10-860-761-3
: Sequence 3, Application US/10860761
: Publication No. US20040248775A1
: GENERAL INFORMATION:
: APPLICANT: WYETH
: TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
: FILE REFERENCE: AM101318
: CURRENT APPLICATION NUMBER: US/10/860,761
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 3
: LENGTH: 3885
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS

Db 2546 TGAAGGAGAGAGATGTAAGATGGCGTGTGAAGCCCTTAAACACCCAAAGTTTGTGG 2605
Qy 777 TUSerLeuArgLeuAspCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnI 797
Db 2666 AGCTTTAGAGCTGATTCGTGTGATGAGCCCAATGCTGTTCCTGAAAGATCTCCAA 2665
Qy 797 TLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyValAsnValThrAspG 817
Db 2666 TCCTTAACAGACCTCCCGACGCTGAAATCTGTAGCCTGGCAGAAACAAGGTGACAGACC 2725
Qy 817 TnglyValMet-ProLeuSerThrAlaLeuArgValIleSerGlnCysAlaLeuGlnLysLeu 836
Db 2726 AGGGATGAC-GCCCTCAGATGATCCCTTAGGGCTCCCAAGTGGCCCTGAGAAAGCTG 2784
Qy 837 TleLeuAspAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuVal 856
Db 2785 ATACTGAGAGATGTGGCATCACACCGGCTTCCAGAGTCTGGCTCAGCCCTCGTC 2844
Qy 857 SerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyVal 876
Db 2845 AGCAACCGAGCTTACACACCTGTGCTTATCCAAACAAGCTGGGAGAGAGTGTGA 2904
Qy 877 AsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsn 896
Db 2905 AATCTACTGTGTGCATTCATGAGGTGCTCCCACTGTAGTCTGCAGAGCTGATGTGAT 2964
Qy 897 GlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLeuAlaLeuMetGlyAsnSe 916
Db 2965 CAGTGCACCTGGACACCGGCTGGCTGTGG-TTCTTTGCACTTGGCTTAAGGATCTC 3023
Qy 916 TTrpleuThrHisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValLysLeuLe 936
Db 3024 ATGGCTGACGACCTGAGCCTTAGATGAACTCTGGAAAGCAATGGCGTAGCTTCT 3083
Qy 936 uCysGlnValMetArgGluProSerCysHisLeuGlnAspLeuGlnLeuValLysCysHis 956
Db 3084 GTGCAGGTGCATGAGAGAACATCTGTCTATCTCCAGACCTGGAGTGTGAAGTGTCA 3143
Qy 956 sLeuThrAlaAlaCysGlySerLeuSerCysValIleSerArgSerArgHisLeuLys 976
Db 3144 TCTACCCCGGCTGTGTGAGAGTCTGTCTGTGTGATCTCGAGAGACAGACCTTAA 3203
Qy 976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlu 996
Db 3204 GAGCTGTGATCTCAAGCAATGCCCCTGGTGAAGGTGGGTGTGCTGGCTGTGGAGGG 3263
Qy 996 YLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016
Db 3264 ACTGAAAGCAAAAGACAGTGTCTGACAGACTCGGGTGTGAAGGCAATGTGACTGACTTC 3323
Qy 1016 TAspCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAs 1036
Db 3324 TGTATGCTGTGAGGACTCTCTCTGGCCCTTCTCTGCAACCGGCAATCTGACACTTAA 3383
Qy 1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCy 1056
Db 3384 CTGTGTGAGATATACCTCAATGCCCAAGGAATGATGAAGCTGTGTGGCTTGGCTGG 3443
Qy 1056 sProThrSerAsnLeuGlnIleLeuGlyLeuThrLysTrpGlnTyrProValGlnIleAr 1076
Db 3444 TCCCACTGTCTAATTAAGATTAATGGCTGTGGAAATGAGCACTGCTGTGCAATTAAG 3503
Qy 1076 GlyLeuLeuGlnGlnValGlnLeuLeuLysProArgValValIleAspGlySerThrHis 1096
Db 3504 GAAAGTGTGAGAGAGAGTGAAGTGAAGTGAAGCCCGAAGTGTGAAGTGAAGTGGCA 3563
Qy 1096 sSerPheAspGlnAspAspArg 1103
Db 3564 TTCTTTTATGATGAAGTGAACCGG 3585

RESULT 8
US-10-399-443-23

; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 616.00 Matches: 1002
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 4
Query Match: 45.83% Indels: 8
Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)
Qy 98 TleSerGlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnGlnIle 117
Db 568 ATTTCAACAAGCTAAGAACAAAGAGGTGCCACAGCAGACAGACAGAACAAAGAAATT 627
Qy 118 SerGlnAlaMetGlnGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnGlnIle 137
Db 628 TCACAAGCTAAGAACAAAGAGGTGCCACAGCAGACAGACAGAACAAAGAAAGTGA 687
Qy 138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGlnGlnGlnAspVal 157
Db 688 GGTACACATGGGACTCAAGAGTCAAGTGTGATGACCAAAATTCGCTGAGAGAGAGATGTA 747
Qy 158 ArgArgSerPheGlnAsnThrAlaAlaAspTrpProGlnMetGlnThrLeuAlaGlyVala 177
Db 748 CGTGTAGTTTGAACAACATGCTGTGACTGCGCGGAAATGCAAAAGTGGCTGGTGGCT 807
Qy 178 PheAspSerAspArgTrpGlyPheArgProArgThrValaIleuHisGlyLysSerGly 197
Db 808 TTTGATTCAGACCCGCTGGGCTTCCGCTGCAACGCTGTTCGACAGAAATCTCAGA 867
Qy 198 TleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217
Db 868 ATGGGAAATCGGCTTAGCCAGAAAGATCGTGTGTGGCGGCAAGGTGAGACTTAC 927
Qy 218 GlnGlyMetPheSerTyrValaPhePheLeuProValArgGlnMetGlnArgLysGln 237
Db 928 CAGGAAATGTTCTCTACGTCCTTCTTCTCCCTTGAAGAGTGAAGCGGAAAGAGAG 987
Qy 238 SerSerValThrGlnPheIleSerArgGlnTrpProAspSerGlnAlaProValThrGln 257
Db 988 AGCAGTGTACAGAGTTCATTCAGAGAGTGGCAGACTCCAGGCTCCGCTGACGAG 1047
Qy 258 TleMetSerArgProGlnArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277

Db	1048	ATCATGTCCGACCGAAGAGCGTGTGTTTCATCTAATGACGTTTCGATGACTGGGCTCT	1107
Oy	278	ValLeuAenAenAaspThrLysLeuCYaLYsaapITPalaGluLYgInProPheTheThr	297
Db	1108	GTCTCCACAAATGACAAAGCTCTGCAAGAGCTGGGCTGAGAGCAAGCTCCGTTACCC	1167
Oy	298	LeuILEaGserLeuLeuAArgLYaValLeuLeuProGluSerPheLeuILEaLThrVal	317
Db	1168	CTCAATACCAAGCTCTGACTAGGAAGGCTCTGCTCCCTGAGTCTTCCTGATGTCACCGTTC	1227
Oy	318	ArgAapValaGlyThrGluYsLeuLYsSerGluValaLserProArgTYrLeuLeuVal	337
Db	1228	AGAGACGTGGGACAGAGAGCTCAAGTCAAGAGGTCTGTTCTCCCGCTTACCTGTAACTT	1287
Oy	338	ArgGlyILEserGlyGluGlnAArgILEhISLeuLeuLeuGluAArgGlyLEGLYgLuHIS	357
Db	1288	AGAGGAACTCCGGGGGAACAAGATTCACCTTGCTCTTGAGCGCGGGATTGGTAGAGAT	1347
Oy	358	GlnLYthrGlnGlyLeuAArgaLAlleMet-AsnAenAArgLUeLeuAapGlnCYaG	377
Db	1348	CAGAAAGACAAAGGGTTGCTGGTCCATCAT-CAACAAACGTAGAGCTGCTGCACAGTCCCA	1406
Oy	377	nValProhAlaValGlySerLeuILECYaValaLeuGlnLeuGlnAapValaGlyG	397
Db	1407	GGTGGCCCCCGGGCTCTCTCATCTGCTGGGCCCCGTGAGCTGACGAGCGTGGGGGGA	1466
Oy	397	uSerValaLapPheAenGlnThrLeuThrGlyLeuHISaLAlaPheVal-PheHISg	417
Db	1467	GAGGTGCCCCCTTCAACAAACGCTCAAGCGCTGACCCCGCTTTGC-GTTTCATC	1525
Oy	417	LnLeuThrProArgGlyValaValaArgaCYsLeuAenLeuGluGlnAArgValaLeuL	437
Db	1526	AGCTCACCCCTCGAGGCGTGGTCCGGCGCTCTCTCAATCTGAGAAAGATTGTTCTCTGA	1585
Oy	437	YsaGAPheCYaArgMetAlaValaGluGlyValaLTPAenAArgLYsSerValaPheAapGlyA	457
Db	1586	AGCGCTTTCGGGATGGCTGGAGGGAGGTGGAAATGAGAAAGCATGTTATGATGATG	1645
Oy	457	sPAapLeuMetValaGlnLYleuGlyGluSerGluLeuAArgaLaleuPheHISmetAsnI	477
Db	1646	ACGACCTCATAGTTCAAGAACTCGGGAGAGTCTGAGCTCCGTCCTGTTCACTGAACA	1705
Oy	477	LeLeuLeuProAapSerHISCYsGluGluLYrTYrThrPhePheHISLeuSerLeuGlnA	497
Db	1706	TCTTCTCTCCACAGACGCACTGTGAGGAGTACTAACCTTCTTCCACCTCAGTCTCCAGG	1765
Oy	497	sPhePheCYaLAlaLeuTYrTYrValLeuGluGlyLeuGluLILEGluProAlaLeuCYaP	517
Db	1766	ACTTCTGTGGCGCTGTACTACGTTGATGAGGGCGCTGGAAATGAGCAAGCTCTCGCC	1825
Oy	517	roLeuTYrValaGluLYthrLYsaPrgSerMetGluLeuLYsGlnAlaGlyPheHISrILEh	537
Db	1826	CTCTGTACGTTGAGAAAGCAAGAGTCTATGAGACTTAACACGCAAGCTTCCATATCC	1885
Oy	537	lAsSerLeuTYrMetLYsaPrgPheLeuPheGlyLeuValaSerGluAapValaArgaProl	557
Db	1886	ACTGCGTTTGAATGAAGCGTTTCTTGTTGGCTCTGTAGGGAAGATGAAGAGGGCAC	1945
Oy	557	eugLIuValLeuLeuGlyCYaProValaProLeuGlyValaLYsGlnLYsLeuLeuHISrTPV	577
Db	1946	TGGAGGTCTCTGCTGGCTGTCCCGTCTCCCGGGGGGTGAAGCAAGCTTCTGACATGGG	2005
Oy	577	AlSerLeuLeuGlyGlnGlnProAenAlaThrThrProlGlyAAspThrLeuAapLAlaPheH	597
Db	2006	TCTCTCTGTGGGTACGACGCTTAATGCCACACCCAGAGACACCTTGAGCCCTTCC	2065
Oy	597	lAsCYsLeuPheGluThrGlnAapLYsGluPheValaArgLeuAlaLeuAenSerPheGlnG	617
Db	2066	ACTGTCCTTTTGAGAGCTCAAGCAAAAGGTTGTTCGCTGGCATTTAAACAGCTTCCAG	2125
Oy	617	luValaLTPLeuProLILEaGlnAenLeuAapLeuLlaleAsrSerPheCYsLeuGlnH	637

Db	2126	AAAGTGGGCTCCGATTAAACGAAACCTGGACCTTGATAGCATCTTCCTGCTCCAGC	2185
QY	637	ISQSPRYTLEuARGLYSILEARGVALARPVALYSGYLIEPhePROARGSPGIUS	657
Db	2186	ACTGCCCCGTAATTTGGGAAAATTTGGGGGTGATGCAAGGGATCTTCCCAAGAGATGATG	2245
QY	657	ERTLAGLUALCYSPROVALVALPROLeUTPMEtARGARYLThREuLIEGLUGUS	677
Db	2246	CCGCTGAGGCGAATGCTCTGTGGTCCCCCTATGAATGGGGAATMAAGCCCTCATTTAGAGAC	2305
QY	677	INTPGLIAPSPheCYSerMetLeuGLIYTHRIspROHILEuARGILEuAPLeUG	697
Db	2306	AGTGGGAAGATTTCTGCTCCATGCTTGGCAACCCACACCTCGCGAGCTGGACCTGG	2365
QY	697	LYSerSeriLEuThRGLuARGLAMELYSTHREuCYVALYLYLeuARGHISPROT	717
Db	2366	GCAGAGCATCTTGACAGAGCGGCGCATGAAGACCTGTGTGGCCAGCTGAGCATCCCA	2425
QY	717	hRYSLYGLIEGLIThREuMetPheARGANALAGNILEThPROGLIYALGINHISL	737
Db	2426	CCTGCAAAATYCAAGCCCTGATGTTTGAATGAATGACAGATTAACCTCGGTGTGCAACCC	2485
QY	737	EUTPARGIIEVALMetALABNARGANLeuARGSerLEuANLeuGLIYGLIYTHRIsl	757
Db	2486	TCGTGAGAAATGTCAATGGCCAAACCGTAACTTAATTCCTCACTTGGAGGACCCACC	2545
QY	757	EULYSGIULIAPSPVALARGMetALCYSGIUALALEuLYHISPROLYSCYLeuLeUG	777
Db	2546	TGAAGGAAGAGATGAAGATGAGTGGCGTGAAGCCTTAAGAACCCCAAAATGTTGTGG	2605
QY	777	IUSerLEuARGLeuAPSPCYSGIYLeuTHRIHALACYTYLeuLYSILESerGLNI	797
Db	2606	AGCTTTGAGGCTGATTTGGTGTGGAATTGACCCATGCTGTTCCTTAAGATATCCCAAA	2665
QY	797	LEuThRThSerPROSerLeuLYSLeuSerLEuALAGLYASNLYEVALThRAPSP	817
Db	2666	TCTTTCAGACCTCCCCAGCCTGAATCTCTGACCTGGCAGGAACAAGGTGACAGACC	2725
QY	817	INGLYValMet-PROLeuSerASPALeUARGVALSerGINCYVALALEuGLNYLeu	836
Db	2726	AGGAGGTAAAC-GCCGTCAAGTAAAGCCTTGAGGGTCTCCAGTGGCCGCTGCAAGCTG	2784
QY	837	IILEuGLIuAPSPCYSGIYIEThRALIThRGLIYCYSGINSerLEuALASERIALeUVAL	856
Db	2785	ATACTGGAGGACTGTGGGATCAACAGCCAGGGTCCAGAGTCTGGGCTCAGCCCTGCTC	2844
QY	857	SERANARGSerLEuThRIALeUICYLeuSerANPMErLEuGLIYANNGIULYVAL	876
Db	2845	AGCAACCGGAACCTTGACACACTGTGTGCTTAACCAACAGCCTGGGGAACGAAGGGTGA	2904
QY	877	ABNLeuLeUCYBARGSerMetARGLeuPROHISCYSerLEuGINARGLeuMetLEuASN	896
Db	2905	AATCTACTGTGTCCATTCATGAAGCTTCCCACTGTGTGTGCAAGAGGCTGATGCTGAAT	2964
QY	897	GLINCYHISLeuAPThRIALGLIYCYSGIYPhe-LEuALLeuUALeUwETGLYANSE	916
Db	2965	CAGTGGCACTGGACACAGGCTGGCTGTGG-TTCTCTTGCACTTGCGCTTATGGGTAACTC	3023
QY	916	RTTPLeuThRIALeUSerLEuSerMetANPProVALIULuAPASNLYVALYLYLeuLE	936
Db	3024	ATGGCTAGCGACCTGAGCCTTGAACGAACCCCTGTGAAGACAAATGGCCGTGAAGCTTCT	3083
QY	936	UCYSGIULIValMetARGIUPROSerCYHISLeuGLIAPLeuGLIYLeuVALYLYCYBHIS	956
Db	3084	GTCGAGGTCAATGAGAAACCATTTGTCACTCCAGAGCTGGAGTTGGTAAAGTCA	3143
QY	956	SLeUThRIALALCYSPCYSGINSerLEuSerCYVALIIESerARGSerARGHISLeuLY	976
Db	3144	TCTCAACGCGCGGTGTGATGAGATGTCTCTGTGTATCTCAGAGGACAGACACCTGAA	3203
QY	976	BSerLEuAPLeuThRAPASNALALEuGLIYAPSPGLIYVALIALALEuCYSGIULI	996
Db	3204	GAGCTGTGATTTCAACGACAAATGCCCTGGGGTGAAGGTGGGGTGTGCAGCTGTGGCAGGG	3263

QY 996 YLeuLysGlnLysAlaSerValLleuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016
DB 3264 ACTGAAGCAAAAGAAAGAGTGTTCGACGAGACTCGGGTTGAAGGCAATGTGACTGACTTC 3323
QY 1016 TASPCTGCTGATGAGGCACTCTCTTGGCCCTTTCGCAACCGGCACTGACCAAGTAA 1036
DB 3324 TGAATGCTGATGAGGCACTCTCTTGGCCCTTTCGCAACCGGCACTGACCAAGTAA 3383
QY 1036 nLeuValGlnAlaSerPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaC 1056
DB 3384 CTTGGTGAAGAAATTAATCTCACTCCCAAGGAATGATGAGCTGTGCTTGGCTTTCCTG 3443
QY 1056 sProThrSerAlaLeuGlnLleGlyLeuThrLysTrpGlnTrpProValGlnLleAr 1076
DB 3444 TCCACGCTCACTTACAGATTAATTTGGGCTGTGAAATGCGAGTACCTGTGCAAAATAG 3503
QY 1076 GlyLeuLeuGlnLleValGlnLeuLysProArgValAlleAspGlySerTrpHi 1096
DB 3504 GAAGCTGCTGAGGAAAGTGCAGCTACTGAAGCCCGAGTCGTAAATGACGGTATGTGCA 3563
QY 1096 sSerPheAspGluAspAspArg 1103
DB 3564 TTCTTTGATGAAAGTACCGG 3585
RESULT 9
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OR INVENTION: Human Gene Critical to Fertility
; FILE REFERENCES: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIORITY FILING DATE: 2003-10-01
; PRIORITY APPLICATION NUMBER: 60/241,510
; PRIORITY FILING DATE: 2000-10-18
; PRIORITY APPLICATION NUMBER: PCT/US02/09776
; PRIORITY FILING DATE: 2002-03-29
; PRIORITY APPLICATION NUMBER: PCT/US01/10981
; PRIORITY FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23
Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 616.00 Matches: 1002
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 4
Query Match: 45.83% Indels: 8
DB: 17 Gaps: 0
US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)
QY 98 lLeSerGlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnTrpGlnGlnGlnLle 117
DB 568 ATTTCACAAAGCTATGGAACAAGAGGTGCCACAGCAGAGAGAGCAAGAAACAATTT 627
QY 118 SerGlnAlaMetGlnGlnGlnGlnGlyAlaThrAlaAlaGlnTrpGlnGlnGlnGly 137
DB 628 TCACAAAGCTATGGAACAAGAGGTGCCACAGCAGAGAGAGCAAGAAACAAGTGA 687

QY 138 GlyAspThrTrpAspTrpLysSerHisValMetThrLysPheAlaGlnGlnLysVal 157
DB 688 GGTGACACATGAGACTCAAGAGATCAAGTATGACCAAAATTCGCTGAGAGAGAGATGTA 747
QY 158 ArgTrpSerPheGlnAlaThrAlaAlaAspTrpProGlnMetGlnTrpLleAlaGlyAla 177
DB 748 CGTGATGTTTGAACAACATGCTGCTGATCGGCGGAAATGCAAAAGTTGGCTGTGCT 807
QY 178 PheAspSerAspArgTrpGlyPheArgProArgThrValLleuHisGlyLysSerGly 197
DB 808 TTTATTTCAAGCCGATGGGCTTCCGCTTCGACCGGTGTTCTGACAGAAATGACGA 867
QY 198 lLeGlyLysSerAlaLeuAlaArgArgLleValLeuCysTrpAlaGlnGlyLysLeuTr 217
DB 868 ATTGGAATTCGGCTTCAGCAGAAAGATCGTGTGTCGGGCGCAAGGTGACTTAC 927
QY 218 GlnGlyMetPheSerTrpValPhePheLeuProValArgGlnMetGlnArgLysGln 237
DB 928 CAGGAATGTTCTCTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 987
QY 238 SerSerValThrGlnPheLleSerArgGlnTrpProAspSerGlnAlaProValThrGln 257
DB 988 AGCAGTGTACAGAGTTCACTCCAGGAGTGGCCAGATCCAGGCTCCGCTGACGAG 1047
QY 258 lLeMetSerArgProGlnArgLeuLeuPheLleLeAspGlyPheAspAspLeuGlySer 277
DB 1048 ATCATGTCCGACCAAGAAAGCTGTGTTCATCATTAAGGTTTCGATGACCTGGGCTCT 1107
QY 278 ValLeuAsnAsnAspTrpLysLeuCysValAspTrpAlaGlnGlnProProPheThr 297
DB 1108 GTCTTCAACAATGACAAAGCTCTGCAAGATCGGGCTGAGAGCGCTCCCTTCAACC 1167
QY 298 LeuLleArgSerLeuLeuArgLysValLeuLeuProGlnSerPheLleValThrVal 317
DB 1168 CTCAATAGCACTGTGCTGAGAGAGTCTCTGCTCCCTTAAGTCTTCTGATGTACCGTCC 1227
QY 318 ArgAspValGlyTrpGlnLysLeuLysSerGlnValAlaSerProArgTrpLeuLeuVal 337
DB 1228 AGAAGCTGGGCAAGAAAGCTCAAGTCAAGAGTCTGCTCCCGTTACCTGTAGTT 1287
QY 338 ArgGlyLleSerGlyGlnGlnArgLleHisLeuLeuLeuGlnArgGlyLleGlyGlnHis 357
DB 1288 AGAGAAATCTCCGGGGAACAAGATCACTGCTCTTGAAGCCGGGATTTGGACAT 1347
QY 358 GlnLysThrGlnGlnLysArgAlaLleMet-AsnAsnArgGlnLeuLeuAspGlnCysG 377
DB 1348 CAGAAACACAAAGGTTGCTGCAAT-CAACACCGTGAAGTCTCCAGCCAGTCCA 1406
QY 377 nValProAlaValGlySerLeuLleCysValAlaLeuGlnAspValValGlyG 397
DB 1407 GTGCCCCGCGTGGGCTCTTCATCTGCGGCCCTGACGTGAGACCGTGGGGA 1466
QY 397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG 417
DB 1467 GAGCGTGGCCCTTCAACCAAGCTGCACAGGCTGCACGCCCTTTTGC-GTTTCACTC 1525
QY 417 lLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlnLysArgValAlaLeu 437
DB 1526 AGCTTACCCCTTCAGGGGTGGTCCGGGCTGTCTCAATCTGAGAGAAAGTGTCTTGA 1585
QY 437 yAspPheCysArgMetAlaValGlnGlyValTrpAsnArgLysSerValPheAspGly 457
DB 1586 AGGCTTCTGCGGATGCTGTGAGGAGAGTGGAAATGAGATGCTGTTATGATG 1645
QY 457 sPheAspLeuMetValGlnGlyLeuGlyCysSerGlnLeuAspAlaLeuPheHisMetLeu 477
DB 1646 ACGACCTTCATAGTTCAGAGACTCGGGAGTCTGAGCTCCGCTCTCTTTCACATGAACA 1705
QY 477 lLeuLeuProAspSerHisCysGlnGlnTrpTrpPhePheHisLeuSerLeuGln 497
DB 1706 TCTTTCCTCCAGACGCACTGTGAGAGTATCAACTTCTTCACTCACTCACTCAAG 1765

Qy 497 sPhePheValAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCyP 517
Db 1766 ACTCTGTGGCCGCTGTACTAGCTGTAGAGGCGCTGGAATCGAGCAGCTCTGCGC 1825
Qy 517 rOleuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleH 537
Db 1826 CTCTGTAGGTGAGAACAAAGAGGTCATGAGACTTAACAGGAGGCTTCCATATCC 1885
Qy 537 fAsSerLeuTyrMetLysArgPheLeuPheGlyLeuValSerGluLysArgValArgArgProL 557
Db 1886 ACTGCTTTGAGATGAGAGGCTTTCTTTGGCTCTGAGCGAGAACCTTAAGAGGCGCAC 1945
Qy 557 euGluValLeuLeuGlyCyPProValProLeuGlyValLysGlnLysLeuLeuHisTyrV 577
Db 1946 TGGAGGTCCTGCGGCTGTCCCGTTCCTGGGGGTGAGAGAGAGCTTCTGCACTGGG 2005
Qy 577 aLSerLeuLeuGlyGlnGlnProAlaAlaThrThrProGlyLysPheThrLeuLysArgPheH 597
Db 2006 TCTCTGTGTGGGTCAAGAGGCTTAATGACACACCCGAGAGACACCTTGAGCGCTTCC 2065
Qy 597 fAsCyLeuPheGluThrGlnApyLysGluPheValArgLeuAlaLeuLysSerPheGln 617
Db 2066 ACTGCTTTTGAAGACTCAAGACAAAGAGTTGTGCTGGCATTAACAGCTTCCAG 2125
Qy 617 lUValTyrLeuProIleHisGlnAsnLeuAspLeuIleAlaSerSerPheCySLeuGlnH 637
Db 2126 AAGGTGGCTTCCGATTAAACAGAACCTGGAATTGAGCATCTTCTTGGCTCCAGC 2185
Qy 637 fAsCyProTyrLeuLysGlyLysArgValAspValLysGlyTyrPheProArgArgPheLus 657
Db 2186 ACTGTCCGATTATTTGGGAAATTCGGGTGAGTGTCAAGAGGATCTTCCCAAGAGATGAGT 2245
Qy 657 eAlaGluAlaCyPProValValProLeuTyrMetArgAspLysPheThrLeuIleGluGlu 677
Db 2246 CCGCTGAGGCAATGCTCTGTGTGCTCTGATGAGTGGAGATTAAGCCCTCATGAGAGC 2305
Qy 677 lntTyrGluAspPheCySerMetLeuGlyThrHisProHisLeuLysGlnLeuAspLeuG 697
Db 2306 AGTGGAGAGATTTCTGCTCCATGCTTGGCACCCACCCACTGGGGAGGCTGAGACTGG 2365
Qy 697 lYSerSerIleLeuThrGluLysArgAlaMetLysThrLeuCyAlaLysLeuArgHisProT 717
Db 2366 GCACAGACAGACTCTGACAGAGGGGCGCATGAAGACCCTGTGTGCCAAGCTGAGGACTCCCA 2425
Qy 717 hrCyGlyGlyIleGlnThrLeuMetPheArgAlaAlaGlnIleThrProGlyValGlnHisL 737
Db 2426 CCTCAAGATACAGACCTGTGATTGTAGAAATGACAGATTACCCCTGTGTGCAACACC 2485
Qy 737 eUTyrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisL 757
Db 2486 TCTGAGAAATCTCATGAGCCAAACGTAACCTTAAGTCCCTCACTTGGAGAGGACCCACC 2545
Qy 757 euLysGluGluAspValArgMetAlaCyGluAlaLeuLysHisIleProLysCySLeuLeuG 777
Db 2546 TGAAGAGAGAGATGTAAAGATGGGCTGTAAGACCTTAACACCCAAATGTTTGTGG 2605
Qy 777 lUserLeuArgLeuAspCyGlyLeuThrHisAlaCyGlyTyrLeuLysIleSerGlnI 797
Db 2606 AGTCTTGAAGGCTGATGTGTGTGATTAACCCATGCTGTAACTTGAAGATCTCCCAA 2665
Qy 797 lLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrArgP 817
Db 2666 TCTTTAGACCTTCCCCAGCCTGAAATCTTGAAGCTTGGACGAGAAACAGGTGACAGACC 2725
Qy 817 lncLysValMetProLeuSerAspAlaLeuArgValSerGlnCyAlaLeuGlnLysLeu 836
Db 2726 AGGAGGTAAAC-GCCTCTCAGTGAAGCTTGAAGGCTTCCAGTGGGCTCTGAGAAAGCTG 2784
Qy 837 lLeuLeuGluAspCyGlyTyrLeuThrAlaThrGlyCyGlnSerLeuAlaSerAlaLeuVal 856
Db 2785 ATACTGAGGAGCTGTGGCATCAAGCCAGGGTGGCCAGATCTGGCCTCAGCCCTCTGTC 2844
Qy 857 SerAsnArgSerLeuThrHisLeuCySLeuSerAsnAsnSerLeuGlyAlaGlnGlyVal 876

Db 2845 AGCAACCGAGACTTGACACACTGTGCTTATCCAAACAAGCCTGGGAGAGAGAGTGTGA 2904
Qy 877 AsnLeuLeuCyAspSerMetArgLeuProHisCySerLeuGlnArgLeuMetLeuAsn 896
Db 2905 AATCTACTGTGTCCATTCATAGAGGCTTCCCACTGTATCTGCAAGGCTGTATGCTGAAT 2964
Qy 897 GlnCyHisLeuAspThrAlaGlyCySglYphe-LeuAlaLeuAlaLeuMetGlyAsnSe 916
Db 2965 CAGTCCCACTGGACAGGCTGGGCTGTGG-TTCTCTTGCACCTTGGCTTAAGGTAATC 3023
Qy 916 rTyrLeuThrHisLeuSerLeuSerMetAsnProValGluLysArgGlyValLysLeuLe 936
Db 3024 ATGGCTGACGACCTGAGCCTTACATATGAACCTGTGGAGAACATGCGCTGAGAGCTTCT 3083
Qy 936 uCyGluValMetArgGluProSerCyHisLeuGlnApyLysGluLysLeuValLysCyHis 956
Db 3084 GTGCGAGGTCAATGAGAGAACATTTGTCACTTCCAGAGACCTGAGATTGTGAAGTGTCA 3143
Qy 956 sLeuThrAlaAlaCySglYSerLeuSerCyValIleSerArgSerArgHisLeuLys 976
Db 3144 TCTACCGCCCGCTGTCTGTAGAGTCTCTCTGTGTATCTCGAGAGACAGACCTGAA 3203
Qy 976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCySglGlu 996
Db 3204 GAGCCTGGATCTCAAGCAATGCCCTGGGTGAGCGTGGGCTTCTGCGCTGTGCGAGGG 3263
Qy 996 lYLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLysLysValaCySglYLeuThrSe 1016
Db 3264 ACTAAGAGAAAGAACAGTGTGTGACAGACTGGGTGAAGGCAATGTGACTGACTTC 3323
Qy 1016 rAspCySglYAlaLeuSerLeuAlaLeuSerCyAsnArgHisLeuThrSerLeuAs 1036
Db 3324 TGATTGCTGTAGAGCACTCTCTTGGCCCTTCTCTGCAACGGCATCTGACCAAGCTTAA 3383
Qy 1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCySeralAphaAlaCy 1056
Db 3384 CCTGTGCAAGATATCTTCACTCACTCCAAAGAAATGAAAGCTGTGCGCTTGGCCG 3443
Qy 1056 sProThrSerAsnLeuGlnIleIleGlyLeuTyrPheGlnTyrProValGlnIleAr 1076
Db 3444 TCCCACTGTAACTTAACATTAATTTGGCTGTGAAATGAGAGAACCTGTGCAAAATAG 3503
Qy 1076 GlYLeuLeuGluGluGluValGlnLeuLeuLysProArgValAlaAspLysSerThrHis 1096
Db 3504 GAAGCTGTGAGAGAGAGTCAAGTACTTCAAGCCCGAGTGTAAATTAACGGTATGTGCA 3563
Qy 1096 sSerPheAspGluAspAspArg 1103
Db 3564 TTTCTTTGATGATGATGACCGG 3585

RESULT 10
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US2004028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.: 0 Length: 1157
Score: 385.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.65% Indels: 0
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)
QY 252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGly 271
Db 1 CAAGCTCCGGTACGGAGATCATGTCCGACCAAGAAAGGCTGTTGTTTCATCATGACCGT 60
QY 272 PheAspAspLeuGlySerValIleuAsnAsnAspThrIleuCyblyAspTrpAlaGlu 291
Db 61 TTCGATGACCTGGGCTGTCTCTCAACAATGACAAAGCTCTGCAAAAGACTGGGCTGAG 120
QY 292 LysGlnProProPheThrIleuIleArgSerLeuLeuArglyValLeuLeuProGluSer 311
Db 121 AAGCAGCCTCCGTTCACTCATACGCACTGCTGAGAGAGGCTCTGCTCCCTGAGTCC 180
QY 312 PheLeuIleValThrValArgAspValGlyThrGluIleuIleuIleuSerGlyValIleSer 331
Db 181 TTCCTGATCGTACCGTACAGAGACGTGGGCAAGAAAGCTTCAAGTCAAGAGGTGCTCT 240
QY 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleIleIleLeuLeuGlu 351
Db 241 CCCCGTACCTGTTAGTTAGAGAAATCCCGGGGAAACAAAGATCCATTCCTCTTGAG 300
QY 352 ArgGlyIleGlyGluIleGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 371
Db 301 CGCGGATTTGGTGCATCAGAAAGACAAAGGCTGCTGCAATCATGAAACCGTGAAG 360
QY 372 LeuLeuAspGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 391
Db 361 CTGCTCGACAGTGCAGAGTGCCTGCGGCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 420
QY 392 GlnAspValIleGlyGluSerValIleProPheAsnGlnThrIleuIleuIleuIleuIleu 411
Db 421 CAGGACGCTGCTGGGAGAGGCTGCTGCTTCAACCAAGACCTGACAGGCTGACGCTG 480
QY 412 AlaPheValPheIleGlnLeuThrProArgGlyValValArgArgCybLeuAsnLeuGlu 431
Db 481 GCTTTTGTGTTCACTCAAGCTCACTCGAGGCGGTGCTCGGCGCTGTCTCAATCTGGAG 540
QY 432 GlnArgValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 451
Db 541 GAAAGAGTTGCTCGAAGCGCTTCTGCGGTAGGTGAGGAGGTGGAATAGAGAG 600
QY 452 SerValPheAspGlyAspAspLeuMetValGlnIleuGlyGluSerGlyLeuArgIle 471
Db 601 TCACTGTTTGAACGCTGACGACTCATGCTCAAGGACTCGGGAGCTGAGACTCCGCTCT 660
QY 472 LeuPheIleMetAsnIleLeuLeuProAspSerHisCybGluGluIleuIleuIleuIleu 491
Db 661 CTGTTTCACTGACATCTCTCTCCAGACAGCCCTGAGAGAGTACTACACCTTCTTTC 720
QY 492 HisLeuSerLeuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 511
Db 721 CACCTCACTTCCAGGACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 512 GlnProAlaLeuCybProLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 531
Db 781 GAGCAGCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 532 AlaGlyPheHisIleHisSerLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 551
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Db 841 GCAGCTTCCATATCACTGCTTTGATGAGAGCGTTTCTTTGCTCGGCTCGAGCGAA 900
QY 552 AspValArgArgProLeuGlnIleuIleuGlyCybProValProLeuGlyValIleGln 571
Db 901 GAGCTAAGAGGCGCAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 572 LysLeuLeuHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 591
Db 961 AAGCTTTCGACCTGGGCTCTCTGTTGGTCCAGCAGCGCTATGTCACACCCAGAGAG 1020
QY 592 ThrLeuAspAlaPheHisCybLeuPheGluThrGlnAspIleuIleuIleuIleuIleu 611
Db 1021 ACCCTGAGCGCTTCCACTGCTCTTTTCAAGACTCAAGACAAAGATTGTTGCTGCTGCA 1080
QY 612 LeuAsnSerPheGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 631
Db 1081 TTAAACAGCTTCCAAAGAGGTGGCTTCGATTAAACAGAACTGAGCTGATGACATCT 1140
QY 632 SerPheCybLeuGln 636
Db 1141 TCCTTCTGCTCCAG 1155

RESULT 11
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; represented by the Secretary of the Department of Health and
; Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677, 943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241, 510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.: 0 Length: 1157
Score: 385.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.65% Indels: 0
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)
QY 252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGly 271
Db 1 CAAGCTCCGGTACGGAGATCATGTCCGACCAAGAAAGGCTGTTGTTTCATCATGACCGT 60
QY 272 PheAspAspLeuGlySerValIleuAsnAsnAspThrIleuCyblyAspTrpAlaGlu 291
Db 61 TTCGATGACCTGGGCTGTCTCTCAACAATGACAAAGCTCTGCAAAAGACTGGGCTGAG 120
QY 292 LysGlnProProPheThrIleuIleArgSerLeuLeuArglyValLeuLeuProGluSer 311
Db 121 AAGCAGCCTCCGTTCACTCATACGCACTGCTGAGAGAGGCTCTGCTCCCTGAGTCC 180
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Qy 312 PheLeu11Val1ThrVal1ArgAspVal1GlyThrGlyLeuLeuSerGluVal1Ser 331
Db 181 TTCCTGATGTCACCGTCAGAGACGTGGGACACAGAGAGCTCAAGTCAAGGTCGTCT 240
Qy 332 ProArgTyrLeuLeuVal1ArgGly1LeuSerGlyGluGlnArg1LeuLeuLeuGlu 351
Db 241 CCCGGTACCGTGTAAAGTAAAGGAATCTCCGGGAAACAAAGATCCATCTGCTCTAG 300
Qy 352 ArgGly1LeuGlyGlu1Gln1GlyThrGlnGlyLeuArg1LeuMetAspAsnArgGlu 371
Db 301 CGCGGATTTGGTGGACATCAGAAAGACAGAGGTTGGTGGATGATTAACACCTGAG 360
Qy 372 LeuLeuAspGlnCyGlnVal1ProAlaVal1GlySerLeu1LeuCyVal1AlaLeuGln 391
Db 361 CTGCTGCACGATGTCAGGTGCGCGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 392 GlnAspVal1Val1GlyGlnSerVal1AlaProPheAsnGlnThrThrGlyLeu1Ala 411
Db 421 CAGACGTGGTGGGAGAGCGTCCGCCCTTCAACAAACGCTCAACAGGCTGACCGC 480
Qy 412 AlaPheVal1Phe1GlnLeuThrProArgGlyVal1Val1ArgArgCyLeuAsnLeuGlu 431
Db 481 GCTTTGTGTTTCATCAGCTCAACCTTCAGGCGTGGTCCGCGCTGCTCATCTGAG 540
Qy 432 GlnArgVal1Val1LeuArgArgPheCyArgMetAlaVal1GlyVal1TrpAsnArg1Leu 451
Db 541 GAAGAAGTGTCTGTAAGCGCTTCCGCTATGCTGAGAGGAGTGTGGAATAGAGAG 600
Qy 452 SerVal1PheAspGlyAspAspLeuMetVal1GlnGlyLeuGlyGlnSerGlyLeuArg1Ala 471
Db 601 TCAGGTGTGACGCGTGAACGACCTCATGTTCAAGACATCGGGGAGTCAAGCTCGCTCT 660
Qy 472 LeuPhe1MetAsn1LeuLeuProAspSer1LeuGlnGlyTyrThrPhePhe 491
Db 661 CTGTTTCACAGAACATCTTCTCCAGACAGCCATGAGAGATCTACCTTCTTC 720
Qy 492 HisLeuSerLeuGlnAspPheCySer1Ala1AlaLeuTyrTyrVal1LeuGlnGlyLeuGln 511
Db 721 CACCTCAGCTCCAGGACTTCTGTCGCGCTTGTATCATGTTTGAAGGCTGGAATC 780
Qy 512 GlnProAlaLeuCyProLeuTyrVal1GlyLeuThr1LeuArgSerMetGluLeu1Gln 531
Db 781 GAGCAGCTCTCTGCTCTGCTGACCTGAGAGAGCAAGAGGCTTCAAGCTTAAACG 840
Qy 532 AlaGlyPhe1Gln1HisSerLeuThrMetLeuArgPheLeuPheGlyLeuVal1SerGlu 551
Db 841 GCAGGCTTCATATCCACTCGCTTGGATGAAGCGTTCCTGTTGGCTGCTGAGCGAA 900
Qy 552 AspVal1ArgArgProLeuGluVal1LeuLeuGlnCyProVal1ProLeuGlyVal1LeuGln 571
Db 901 GACCTTAAGAGAGCCACTGAGGCTCTGCTGCGCTCTCCCTTCCCTGCGGTGAGAGC 960
Qy 572 LysLeuLeu1His1TrpVal1SerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591
Db 961 AAGCTTTCGACATGGGTCTCTCTGTTGGGTGAGCAGCTTAATGCCACACCCAGAGAAC 1020
Qy 592 ThrLeuAspAlaPheHisCyLeuLeuPheGlnThrGlnArg1LeuPheVal1ArgLeuAla 611
Db 1021 ACCCTGACGCGCTTCCACTGCTTTCAGAGCTCAAGAGCAAGAGTTTGTCTGCTGCA 1080
Qy 612 LeuAsnSerPheGlnGluVal1TrpLeuPro1LeuGlnAsnLeuAspLeu1Leu1Asp 631
Db 1081 TTAACAGCTTCCAAAGAGTGTGCTTCCGATTAACAGAACCTGAGCTTATAGCATCT 1140
Qy 632 SerPheCyLeuGln 636
Db 1141 TCCTTCTGCTCCAG 1155

RESULT 12
US-10-399-443-3
; Sequence 3, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-3

Alignment Scores:
Pred. No.: 1,19e-192 Length: 1075
Score: 196.00 Matches: 252
Percent Similarity: 99.21% Conserved: 0
Best Local Similarity: 99.21% Mismatches: 1
Query Match: 14.58% Indels: 2
Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-3 (1-1075)

Qy 851 Leu1Asp1AlaLeuVal1SerAsnArgSerLeuThrHisLeuCyGlnSerAsnAspSer 870
Db 2 CTGGCTTCAAGCTCTGCTGACAGACCGGAGCTTGAACACCTGTGCTATCCAAACAGC 61
Qy 871 LeuGlyAsnGlnGlyVal1AsnLeuLeuCyArgSerMetArgLeuProHisCySerLeu 890
Db 62 CTGGGAAAGAGGTGTAATCTATCTGTGTGATCTCATGAGGCTTCCCACTGATGCTG 121
Qy 891 GlnArgLeuMetLeuAsnGlnCyHisLeuAspThrAlaGlyCyGlyPhe-LeuAla 910
Db 122 CAGAGCTGATGCTGAATCAGTGCACCTGACAGCGGTGCTGAG- TTCTTGGCACT 180
Qy 910 ValLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVal1GluAs 930
Db 181 TGCGCTTAATGGGTAACTCATGCTGACGACCTGAGCCTTGAATGAACCTGTGAGAGA 240
Qy 930 PAsnGlyVal1LysLeuLeuCyGlnVal1MetArgGluProSerCyHisLeuGlnAspLe 950
Db 241 CAATGGCGTGAAGCTCTGTGTCAGAGTCTATAGAGAACATCTTGTATCTCCAGAGCT 300
Qy 950 GlnLeuVal1LysCyHisLeuThrAlaVal1CyGlnSerLeuSerCyVal1Leu 970
Db 301 GGAATTTGGTAAAGTATCATCTCACCGCGCGTGTGAGAGTGTCTGTGTGATCTC 360
Qy 970 PArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyVal1 990
Db 361 GAGAGCAGACCACTGAAGAGCTGAGATCTCAACGACATCCCTGGGTGACGCGTGGGT 420
Qy 990 LAlaLeuCyGlnGlyLeuLysGlnLysAsnSerVal1LeuThrArgLeuGlyLeu 1010
Db 421 TGCTGCGTGTGCGAGGAGTGAAGCAAAAGAGTGTGACAGACCTGGGTTGAA 480
Qy 1010 SalCyGlnGlyLeuThrSerAspCyGlnVal1LeuSerLeuAlaLeuSerCyAsnArg 1030
Db 481 GGCATGTGACATGACTTGTATGCTGTGAGGCACTCTCTTGGCCCTTCTCAACCG 540
Qy 1030 GHisLeuThrSerLeuAsnLeuVal1GlnAsnAspSerProLysGlyMetMetLysGle 1050
Db 541 GCATCTGACAGTCTAAACCTGTGAGAGAAATTAATTGCTCCAAAGAAATGAGAGCT 600

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Oy 1050 uCyseRAlaPheAlaCyseProThSerAenLeuGlnIleIleGlyLeuTrpI 1070
Db 601 GTGTCGGCTTGTGCTTCCACGCTTAACATAATATGGCGCTGGAATGSCA 660
Oy 1070 nTyProValGlnIleArgLyLeuLeuGluIuValGlnLeuLeuLyProArgVal 1090
Db 661 GTACCTGTGTGAATAAGAGAGCTGTGAGAGAGTGAAGTGAAGTCAAGCCCGAGTGT 720
Oy 1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
Db 721 AATTGACGGTAGTGTGCAATCTTTTGATGAGATGACCGG 760

RESULT 13
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-3

Alignment Scores:
Pred. No.: 1,19e-192 Length: 1075
Score: 196.00 Matches: 252
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 1
Query Match: 14.58% Indels: 2
Gaps: 0
DB: 17

US-10-066-521-6 (1-1344) x US-10-677-943-3 (1-1075)
Oy 851 LeuAlaSerAlaLeuValSerAenArgSerLeuThrHisLeuCyLeuSerAenAsnSer 870
Db 2 CTGGGCTTACGGCCCTGCTGAGCAACCGAGCTTGACACACCTGTGCTTCCAAACACAGC 61
Oy 871 LeuGlyAsnGluGlyValAsnLeuLeuCyAsnSerMetArgLeuProHisCySerLeu 890
Db 62 CTGGGGAACGAGGCTGAATCTACTGTGATCCATGAAGCTTCCCACTGAAGTCTG 121
Oy 891 GlnArgLeuMetLeuAsnGlnCyHisLeuAspThrAlaGlyCyGlyPhe-LeuAlaLe 910
Db 122 CAGAGGCTGATGCTGAATCACTGACCACTGAGCAACGGCTGCTGTGG-TTCTCTTGCACT 180
Oy 910 uAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAs 930
Db 181 TGGCCTATATGGTAACTCATGAGCTGACGCACTGAGCTTATGACATGAACCTGTGGAAGA 240
Oy 930 PAsnGlyValAlaLyLeuLeuCyGlyIuValMetArgIuProSerCyHisLeuGlnAspLe 950
Db 241 CAATGGCGTGAAGCTTCTGTGCGAGGTCTATGAGAAACATCTGTCTATCCAGAGACT 300
Oy 950 uGlnLeuValLyCyHisLeuThrAlaAlaCyseGluSerLeuSerCyseValIleSe 970
Db 301 GGAAGTGTAAATGTCAATCTCAACGCGCGGTGCTGTGAGAGTCTGTCTGTGTATCTC 360
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Oy 970 rArgSerArgHisLeuLySerLeuAspLeuThrAspAsnAlaLeuGlyValGlyVal 990
Db 361 GAGGAGGAGACACCTGAAGAGCCGTGATCTACGAGCAAAAGCCCTGGGTGACGCTGGGCT 420
Oy 990 lAlaAlaLeuCyseGluGlyLeuLyGlnLyAsnSerValLeuThrArgLeuGlyLeuLy 1010
Db 421 TGTGCGCTGTGCGAGGAGACTGAAGCAAAAGACAGTCTTCTGACGAGACTCGGGTTGAA 480
Oy 1010 sAlaCyseGlyLeuThrSerAspCyseGlyAlaLeuSerLeuAlaLeuSerCyseAsnAr 1030
Db 481 GGCATGTGACTGACTTCTGATGCTGTGAGGCACTCTCTTGGCCCTTCTCTGCAACCG 540
Oy 1030 gHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLyGlyMetLeuLySe 1050
Db 541 GCATCTACCAAGTCTAAACCTGGGAGAAATACCTTAAGTCCCAAGAAATGATGAAGCT 600
Oy 1050 uCyseRAlaPheAlaCyseProThSerAenLeuGlnIleIleGlyLeuTrpI 1070
Db 601 GTGTCGGCTTGTGCTTCCACGCTTAACATAATATGGCGCTGGAATGSCA 660
Oy 1070 nTyProValGlnIleArgLyLeuLeuGluIuValGlnLeuLeuLyProArgVal 1090
Db 661 GTACCTGTGTGAATAAGAGAGCTGTGAGAGAGTGAAGTGAAGTCAAGCCCGAGTGT 720
Oy 1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
Db 721 AATTGACGGTAGTGTGCAATCTTTTGATGAGATGACCGG 760

RESULT 14
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258159
; LENGTH: 2099
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258159

Alignment Scores:
Pred. No.: 3.52e-48 Length: 2099
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.24% Indels: 0
Gaps: 0
DB: 13

US-10-066-521-6 (1-1344) x US-10-027-632-258159 (1-2099)
Oy 668 MetArgAspLySerThrLeuIleGluGluGlnTrpGluAspPheCyseMetLeuGlyThr 687
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Db 220 ATGGGGATAGACCTCATTGAGGAGGAGGAGATTCTGCTCCATGCTTGACACC 279
Qy 668 H1APROH1SLAUG1LLEUAAPLNUGLYSESRILEUThRLUARG1AMETLYS 707
Db 280 CACCCACACCTGCGGACCTGAGCTGGGACGACATCTGACAGACGGGCCATGAG 339
Qy 708 ThRLUCYSA1ALY1LLEUAARGH1APROTHRCYSLYS1LEG1NThRLUmet 724
Db 340 ACCCTGTGTGCAAGCTGAGGCATCCACCTGCAAGATACAGACCCCTGATG 390

RESULT 15
US-10-027-632-258159

; Sequence 258159, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 258159
; LENGTH: 2099
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258159

Alignment Scores:

Pred. No.: 3.52e-48 Length: 2099
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.24% Indels: 0
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-027-632-258159 (1-2099)

Qy 668 MetARGAPLYSTHRLU1LGLUGLNTTTPGLUAPPHCYSESRMETLEUGLYTHR 687
Db 220 ATGGGGATAGACCTCATTGAGGAGGAGATTCTGCTCCATGCTTGACACC 279
Qy 688 H1APROH1SLAUG1LLEUAAPLNUGLYSESRILEUThRLUARG1AMETLYS 707
Db 280 CACCCACACCTGCGGACCTGAGCTGGGACGACATCTGACAGACGGGCCATGAG 339
Qy 708 ThRLUCYSA1ALY1LLEUAARGH1APROTHRCYSLYS1LEG1NThRLUmet 724
Db 340 ACCCTGTGTGCAAGCTGAGGCATCCACCTGCAAGATACAGACCCCTGATG 390

Search completed: February 5, 2005, 01:22:59
Job time : 1727 secs

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Db 73 CAGCTTCGCTCGCCAAATMAAGCGCATCCAGAGCTTCGCGGTGAGACACCGCTCAG 132
Qy 49 GlutIleuAlaSerValGluCysIleuAlaLeuIleuHiegluTyTrGluVala 68
Db 133 CCAAGAAAGAGAGATGGGATGAGAGTGGCTCTGACTCTGCTGGCTCAG---TATGGGAG 189
Qy 69 SerIleuAlaTrpAlaThrSerIleSerIlePheGluIleuMetAsnIleuArgThrIleuSer 88
Db 190 CAGCGGCTGGGACCTGACCTGCTCATCTGGGAGAGATGGGCTGAGGCTCACTGTGC 249
Qy 89 GluIysAlaArgAspAsp----- 94
Db 250 GCCAAGCCCAAGAAAGGGGAGGCCCATCTCTCATTCCTTCCCTTACAGCCCAAGTGAACCC 309
Qy 94 ----- 94
Db 310 CACCTGGGGTCTCCAGCCAAACCACTTCACCGCAGTGTAAATGCCGTGATCCATGA 369
Qy 94 ----- 94
Db 370 TTGCGGGGGGTGACCCAGGGCTCAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429
Qy 95 -----MetIysIysIleSerGlnAlaMet----- 102
Db 430 TCTGACGCGCTGGAGAGAAATCTGCTCCTCACTCTCAAGCTTCCAAAGCTCC 489
Qy 102 ----- 102
Db 490 CCAAGCATAGTGTCCAGAGCAGAGATCCCAAGCCCCCAATCCACAGCAGTGTCTG 549
Qy 103 -----gluIleuIleuVala--- 107
Db 550 GGGAGCTGGGGATCCCGACCTCAGCCAGCTGACCCAGAGCAGAGAGGCTCTGGG 609
Qy 108 -----ThrAlaAlaGluThrGluIleu 114
Db 610 ACCCAATGGCTCTGATGAACGTCAAGAAATTAATAACAGAAATCAGAAAGAGAG 669
Qy 115 GlnGluIleSerGlnAlaMetGluIleuIleuAlaThrAlaIleuValaIleuIleu 134
Db 670 AGAGAGAAATCAGAGAAAGGAGGCGCCCATGGGAGGGGTGAGAGAACCCCCCAG 729
Qy 135 GluIleuIleuIleu----- 138
Db 730 GCGCAGCAGCAGCTCAGAGCCCAACCAACCATGGAGGCTCTGTGTGAGAGAGCTTC 789
Qy 139 ---AspThrTrpAspTrpIysSerHisValMetThr---LysPhe----- 151
Db 790 TGTTCACATGGCCCTGGAAAAATGAGGATTTTAACAAAATTCACACAGCTGCTACTT 849
Qy 152 -----AlaGluIleuIleuValaArgAspPheGluIleuThr 164
Db 850 CTACAAAGACTCAGCCCAAGAGCCAGATCCCTGGTCAAGAGAGC----- 897
Qy 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
Db 898 -----TGGCTGATATGTGAGAGAGAAATGAGGACATTTAATTGATGATCAGAGAC 948
Qy 174 LeuAlaIleuIleu---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleu 192
Db 949 TTATTGGGCCAGGCTGGATACCCAA-----GAACCTCGCATGTCATCTAGT 996
Qy 193 HiegluIysSerGlyIleGlyIysSerAlaIleuAlaArgAlaIleuValIleuCysTrpAla 212
Db 997 CAGGGGGCTGTGAATTTGGAAATGACACCTGGCCAGGCAAGTGAAGAAAGCCCTGGGGG 1056
Qy 213 GlnGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 232
Db 1057 AGAGGCCAGCTGTATGGGAGCCGCTTCCAGAGATGTTCTTCACTTCAAGTGCAGAGAGCTG 1116
Qy 233 GlnArgIysIysGluIleuSerValThrGluIleuSerArgIleuTrpProAspSerGln 252

Db 1117 GCCAGTCCAAAGGTGTGAGTCTGCTGAGCTCATCCGAAAAAGATGGGACAGCCACTCCG 1176
Qy 253 AlaProValThrGluIleuMetSerArgProGluIleuIleuPheIleuAspGlyPhe 272
Db 1177 GCTCCCATTAACAGATCTCTTAGGAGAGAGGGGCTGCTTTCATCTCTGATGGGTGTA 1236
Qy 273 AsnAspIleuGlySerValIleuAsnAsn---AspThrIleuIleuCysIleuAspTrpAlaGlu 291
Db 1237 GATAGGCCAGGATGGGTCTTTCAGAGAGCCAGTTCGTGAGCTGTGCTGCTGACCTGAGCCAG 1296
Qy 292 LysGlnProProPheThrIleuIleuArgSerIleuIleuArgValIleuIleuProGluIleu 311
Db 1297 CCAAGCCGGCGGATGCACTGTGGCAGTGTGCTGGGAAACATATCTTCCAGAGCA 1356
Qy 312 PheIleuIleuValThrValArgAspValGlyThrGluIysIleuIysSerGluIleuValSer 331
Db 1357 TCTTCTCGATGACAGGCTCGGACCAAGCTGTGAGAAACCTCATTCCTTCTTGGAGAG 1416
Qy 332 ProArgTrpIleuIleuValArgGlyIleSerGlyIleuIleuArgIleuIleuMetAsnAsnArgIleu 351
Db 1417 GCAAGTTGGGTGAGAGTCTGGGGTCTCTGAGTCCAGAGAGAAATATTTCTACAGA 1476
Qy 352 ArgGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 371
Db 1477 TATTTCACAGATGAAGGCAAGCAATTAGAACCTTTAGTGTGGTCAAAATCAAAAGAG 1536
Qy 372 LeuIleuAspGlnCysGluIleuProAlaValGlySerIleuIleuCysValAlaIleuGlnIleu 391
Db 1537 CTCTGGGCGCTGTCTTGTCCCTGGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1596
Qy 392 GlnAspValValGlyIleuSerValAlaProPheAsnGlnThrIleuIleuIleu---Leu 409
Db 1597 CAGATGAAGCGGAGAGAAACTCACACTGACTTCAAAAGCACCACCAACCTCTGTCTTA 1656
Qy 410 HieAlaIleuPheValPheHisGlnIleuThrProArgIleuValAlaIleuArgCysIleuAsn 429
Db 1657 CATTACCTTGCCAGGCTCTCCAGCTCAGCAATGGGA----- 1695
Qy 430 LeuGluIleuArgValIleuIleuArgPheCysArgMetAlaIleuGluIleuValIleuPheAsn 449
Db 1696 -----CCCAAGCTCAGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
Qy 450 ArgIysSerValPheAspGlyAspAspIleuMetValGlnGlyIleuGlyIleuSerGluIleu 469
Db 1744 AAAAAGACCTTTCACTCCAGATGACTCAGAAAGCATGGGTTAGATGGGCGCATATC 1803
Qy 470 ArgAlaIleuPheHisMetAsnIleuIleu-----LeuProAspSerHisCysGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCAACCCATCCCTGTGAGC----- 1854
Qy 486 GluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 505
Db 1855 -----TACAGCTTCACTCACTCTGTTTCCAGAGAGTCTTGTGAGCAATGTCTATGTC 1908
Qy 506 LeuGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 523
Db 1909 TTGAGGATGAGAGGGGAGAGGATTAACATTTATGATGATGATGATGATGATGATGATGATG 1968
Qy 524 LysArgSerMetGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 540
Db 1969 CTAGAACCA-----TATGAAATTAACATGGCTGTGTGGGGCATCA 2007
Qy 541 MetIysArgPheIleuPheGlyIleuValIleuSerGluIleuValArgArgProIleuGluIleu 560
Db 2008 ACCACAGCTTCTCTATTGGGCTGTTAAGATGATGATGATGATGATGATGATGATGATGATG 2067
Qy 561 LeuGlyCysProValProIleuGlyValIleuGlnIleuIleuIleuIleuIleuIleuIleu 580
Db 2068 TTTTACGTGGGCTGTCTGAGGGG-----AGAACTGATGACAGTGGTCCGTCCCTG 2121
Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrIleuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGCTGAGGCAAC-----TCTGAGATGCTCCCTCAGCTGC 2163

APPLICANT: Reed, John C.
TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
FILE REFERENCE: P-LJ 3650
CURRENT APPLICATION NUMBER: US/09/388,221B
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4200
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4197)
US-09-388-221B-3

Alignment Scores:
Pred. No.: 1.83e-90 Length: 4200
Score: 949.00 Matches: 387
Percent Similarity: 35.79% Conservative: 190
Best Local Similarity: 24.01% Mismatches: 458
Query Match: 13.42% Indels: 579
Gaps: 55

US-10-066-521-6 (1-1344) x US-09-388-221B-3 (1-4200)

QY 11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspTyrGlnGluPheGlnThrPhe 29
DB 13 GCGTGGGGCCCGCTGGCTTACTGTGAGTTCCGAAAGAGAGAGCTGAGAGAGTTTC 72
QY 30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48
DB 73 CAGCTTCGTCTCGCCAAATMAAGCGCATCCAGAGAGCTTGGGGTGAGACCCGCTCAG 132
QY 49 GluIleGluAsnValAsnValGluCysLeuAlaLeuLeuHisGluTyrTyrGlyAla 68
DB 133 CCAAGAGAAAGAGAGTGGAGATGAGAGTGGCTCTGTAAGCTGGTGGCTCAG---TATGGGAG 189
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnLeuArgThrLeuSer 88
DB 190 CAGGGGGCTGGAGCTTACCCCTCATACCTGGAGAGAGATGGGGCTGAGGCTCATCTGTC 249
QY 89 GluLysAlaArgAspAsp----- 94
DB 250 GCCCAAGCCGAGAAAGGGGAGGCGCACTCTCTCATTTCCCTTACAGCCCAAGTGAACCC 309
QY 94 ----- 94
DB 310 CACCTGGGGTCTCCAGCCAAACCACTTCAACCGCAGTCTAATGCTTGATTCATGAA 369
QY 94 ----- 94
DB 370 TTGCGGGGGGTGACCCAGGGGCTCAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429
QY 95 -----MetLysLysIleSerGlnAlaMet----- 102
DB 430 TCTGAGCCGCTGAGAGAAATCTGTGCTCACTCTCTCAAGCTTCTTCAAGCTCC 489
QY 102 ----- 102
DB 490 CCAAGCATGAGTCTCCAGCCAGAGATCCCAACGCCCAATCCACAGCAGAGTGTG 549
QY 103 -----GluGlnGluGlyAla--- 107
DB 550 GGGAGCTGGGAGTCCCACTCAAGCCAGCTGAGACCCAGAGAGAGAGGCTCTGGG 609
QY 108 -----ThrAlaAlaGluThrGluGlu 114
DB 610 ACCCAATGGCTCTGATGAACGTCAGGAATTTTACTACACAGAAATCAGAGAAAGAG 669
QY 115 GlnGluIleSerGlnAlaMetGluGlnGluLysAlaThrAlaAlaGluThrGluGln 134
DB 670 AGAGAGAAATCAGAGAAAGGAGAGGCCCTCATGGTGAAGCGGCTGAGAAAGCCCCCAG 729

QY 135 GlyHisGlyGly----- 138
DB 730 GCGCAGCACCAAGCTTACAGCCCAACCAACCATGAGAGCTTCTGTGAGAGAGGCTTC 789
QY 139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe----- 151
DB 790 TGTTTCCATGAGCCCTGAGAAATATGAGAGATTTTACCAAAATTTCAACAGCTCTACTT 849
QY 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
DB 850 CTACAAAGACCTCAACCCAGAGCAGAGATCCCTGGTCAAGAGAGC----- 897
QY 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
DB 898 -----TGGCTGTATTATGTGAGAGAGATTCAGAGACATTTAATGAGATCAGAGAC 948
QY 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProAlaGlnValLeu 192
DB 949 TTATTGGCCCGAGGCTGAGTATACCAA-----GAACTCCCATGATCATACTG 996
QY 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCystrAla 212
DB 997 CAGGGGCTGCTGGAATTTGGGAATCAACATGGCCAGCAGAGTGAAGAGAGAGCTGGGG 1056
QY 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
DB 1057 AGAGGCGAGCTGTATGGGAGACCGCTTCCAGCATCTTCTTCACTTCACTGACAGAGACTG 1116
QY 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
DB 1117 GCCCAGTCCAAAGTGGTGAAGTCTGTGAGCTCATCGAAGAAAGTGGAGACACCATCCG 1176
QY 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleAspGlyPhe 272
DB 1177 GCTCCCATTTAGACAGATCCGTCTAGCCAGAGGGGCTGCTTCACTCCATCCGATGGTGA 1236
QY 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCyLysAspTrpAlaGlu 291
DB 1237 GATGAGCCAGAGATGGGCTTGTGAGAGACCGAGTCTGAGCTGTCTGTGCACTGAGAGCAG 1296
QY 292 LysGlnProProMetThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
DB 1297 CCACAGCCGCGAGATGACATGCTGGGAGATTTGCTGGGAAACTATATATCTCCGAGGCA 1356
QY 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
DB 1357 TCTTCTGATACAGGCTCCGAGCCAGCAGCTGCAAGAACTCATTTCTTCTTGGAGCAG 1416
QY 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGlu 351
DB 1417 GCAGTGGGAGAGGCTCTGGGGTCTCTGAGTCCAGAGAAAGAAATTTTCTACAGA 1476
QY 352 ArgGlyIleGlyHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
DB 1477 TATTTCACAGATGAAGGACCAATTAAGACCTTTAGGTTGGTCAAAATCAAAAGAG 1536
QY 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
DB 1537 CTCTGGGCTGCTGTCTTGTGCTGCTGGTGTCTGGCTGCTGCTGCTGCTGCTGCTGCTG 1596
QY 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409
DB 1597 CAGATGAAGCGAGAGAAATCACTCACTCACTCAAGAACACCAACACCTCTGTCTTA 1656
QY 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValAlaArgArgCysLeuAsn 429
DB 1657 CATTAACCTGCCAGGCTCTCAAGCTCAAGCATTTGGA----- 1695
QY 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
DB 1696 -----CCCAAGCTCAAGAGACCTTGTCTGTGCTGTGCTGAGGGCATCTGGCAA 1743

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Db 1744 AAAAAGACCTTTTCAGTCCAGATGACTCAGAAAGCATGGGTATGATGGGCCATCATC 1803
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATCTTTCAGAGCAGCCCATCCCTCTAGC----- 1854
Qy 486 GluTyrTrpThrPhePheHisLeuSerLeuGlnAspPheCysAlaIleLeuTyrVal 505
Db 1855 -----TACAGCTTCATTCACCTCTGTTTCCAAAGAGTCTTTGACGCAATGCTTATGTC 1908
Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluTyrThr 523
Db 1909 TTGAGAGATGAGAAAGGGAGAGTAAACATTCTAATTCATCATATGATTTGGAAAGACG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyr----- 540
Db 1969 CTAGAGCA-----TATGGATATACATGGCCTTGTGGGCGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACAGCTTTCCTATGAGCTGTTAATGATAGAGGGAGAGAGATGAGAAACATC 2067
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuHisIleTrpValSerLeuLeu 580
Db 2068 TTTTACCTGCGCGGTCTCAGAGG-----AGAACTCGATGAGAGTGGTCCCGTCCCTG 2121
Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGTCGACCCACAC-----TCTCTGAGATCCCTCCACATGC 2163
Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db 2164 TTGTACAGACTCTGGAAACAAACCTTCTCGACACAGTATGGCCCATTTGAAACAAATG 2223
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Db 2284 CGCACAGTGAAGAGCTTCAGCTG-----ATGAGAGGC-----AGCACACAGATCA 2331
Qy 659 GluAlaCysProValValProLeuTrpMetArgArgAspThrLeuIleGluGlnTrp 678
Db 2332 AACATGAGGCCACCATGTGATCTCTGTTCAGTGGGTCCACATGACAGATGCCATATGG 2391
Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLysSer 698
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Db 2391 ----- 2391
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Db 2392 -----CAATTCCTTTC 2403
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyLysThrHisLeuLys 758
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Db 2530 -----TTGGCTGGC----- 2538
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Qy 859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeu 878
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Db 3076 CTCTTGCGCGCTTCTCTCTGCTTCAGAGGAGACTGCACAGAGAACTTTGG----- 3130
Qy 1069 PGIInTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLysProArgVal 1089
Db 3130 ----- 3130
Qy 1089 IValIleAspGlySerTrpHisSerPheAspGluAspArgHisValLysIleGlyLeuThr 1109
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Qy 1109 PheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGly 1129
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Qy 1129 uGlnLysLeuArgValSerLeuLeuAlaGlyAspPheLysSerThrArgPheAlaLys 1149

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Db	3215	-TCCCTGTAGTGGCTGGCTCCCTACCGCTGGCCCAACA--CGGGCTCTGGCTTTGGTAGA		3270
Oy	1169	erSerProGlnProMetLeuIaGlyThnGlnHisAlaGlnAspArguysMetLeuSerValGly-		1188
Db	3271	GAAGGGGTGAC-----	---CGTTGAGATTGAAATCTGTGTGTGGAGC	3309
Oy	1189	--TyrSerGlyAlaIaTrpSerGlnThrAlaGluLeuGlnGlyLeuGlySerAsnSerAlaA		1208
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Oy	1208	sPHisAspHisbelyGlyMetAlaIaTrpSerLeuGlyAlaArgGlyLeuSerSerAlaArgGlyLeuC		1228
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Oy	1228	ys-----ProThrValLeuMetCThrThAlaAlaValCysProGlyHisTrpGluArgLeuG		1246
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Oy	1246	lySerArgGly-----		1249
Db	3474	AGAGAGAGGGAGATGCTCTGGAGAAAGCCAGCGGTGAGCTGCATCATAGTTCTGGA		3533
Oy	1249	-----		1249
Db	3534	AAACCCCAAGCTTCTCCCCCTTGGAGAGTCTCTCTGAATAATGATTCATATATGCCCTGGCGTT		3593
Oy	1250	-----TrpCys-----	LeuAsnSerAlaAspA	1257
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Oy	1257	sPHisSer-----	GlyAlaSerTrpSerLeuGlyAlaA	1268
Db	3654	CCACCTCTACCTGATCCCAAGTGACTGCTCATTTGGAGAAAGAACTGGAGAC-----T		3704
Oy	1268	IaGlyLeuGlnGlyLeuValSerAsnSerAlaAspAspHisSerGlyValAlaA--Trps		1287
Db	3705	CTGCTATGTGAAGCCCTGGAGAAAGACCAAGCTGTTCTTCGAGTTCTACGTTGGCCCACTTGGG		3764
Oy	1287	erLeuGlyAlaA-Ala-----	GlyLeuGlnGlyLeu	1296
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Oy	1297	-----	ValSerAsnSerAlaAspAspHisSerGly	1306
Db	3825	GGTGAACCAAGAGATCTCATGCTCGCAACTACTGATCCCTCCAGGCCGATGCGCT		3884
Oy	1307	-----ValSerTrpSerLeuGlyAlaIaGlyLeuGlnGlyLeuValSerAsnSerAlaA		1324
Db	3885	ACCTTCACTCTGAGATGCCGCGCAGATGTGCACATTTGTGACACATATTCAGAGAGAGCT		3944
Oy	1325	AspAspHisSerGlyValSerTrpSerLeu		1334
Db	3945	GATAGCCCGAGTGCATCGG--TGAGAGTTG		3973

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RESULT 3
US-09-388-221B-5
; Sequence 5, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4332
; TYPE: DNA

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; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4332)
; US-09-388-221B-5

Alignment Scores:
Pred. No.: 1,94e-90
Score: 949.00
Percent Similarity: 36.80%
Best Local Similarity: 24.56%
Query Match: 13.42%
DB: 4
Gaps: 49
Length: 4332
Matches: 359
Conservative: 179
Mismatches: 423
Indels: 502

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OY 30 IyveGIuLeuLeuLybLybLySer---SerGIuSerThaTPrySserIIePheGIuPhne 48
Db 73 CAGCTTGTGTGCTCCCAATTAAGGAGCACTTCAGAGAGCTTGTGGGTGAACACCCGCTCAG 133
OY 49 GIuIIeGIuAaNIaAaNIaGIuCYbLeuAlaLeuLeuLeuNIeGIuTYrTyrGIyAla 68
Db 133 CAGAGAAAGACAGGTGCATGGAGGTGGCTGTACTGTAGGTGCAG--TATGGGGAG 189
OY 69 SerIeuAlaTPraIaThrSerIIeSerIIePheGIuAaMeIaMeIuAaTYrThLeuSer 88
Db 190 CAGCGGGCTGGAGACCTTAAGCCTTCATACCTGGAGAGATGGGGCTGAAGGTCACTGTGC 249
OY 89 GIuIyAaIaArGIaArApArp----- 94
Db 250 GCCCAAGCCAGGAAGGGCAGGGCAGGCACTGTCCCTCATTTCCCTTACAGCCCAAGTGAACC 305
OY 94 ----- 94
Db 310 CACCTGGGTCTCCAGCCAAACCACTTCACCGAGTGTAAATGCCCTGTAGTCATGA 365
OY 94 ----- 94
Db 370 TTGCCGGCGGGGTGCACCCAGGGCTTCAGAGAGAAAGGTTTGAACAGCTGCTGAAC 425
OY 95 -----MetLybLybIIeSerGIuIaMeI----- 102
Db 430 TTGTGAACGCGCTGGAGAAATCTGTGCTCACTCTACCAAGCTTTCAGAGCTCC 489
OY 102 ----- 102
Db 490 CCAAGCAATGATCTCAAGCAAGAGATCAACCAAGCCCCACATCCACAGAGTGTG 549
OY 103 -----GIuGIuGIuGIyAla----- 107
Db 550 GGGAGCTGGGAGATCCCACTCAAGCCAGGCTTGAAGCCCAAGAGAGAGAGAGGCTCTGG 609
OY 108 -----ThraIaAlaGIuThrGIuGIu 114
Db 610 ACCCAATGGCTCTGTGATGAAGAACTCAGGAATTTACTACAGAAATCAGAGAAAGAG 663
OY 115 GIuGIuIIeSerGIuIaMeIeGIuGIuGIyAlaThraIaAlaGIuThrGIuGIuGIu 134
Db 670 AGAGAGAAATTCAGAGAAAGCAGAGGCCCCCACTGGGAGCGGTGTAGGAACGCCCCACAG 722
OY 135 GIyIIeGIyGIy----- 138
Db 730 GCGCACACAGGCTTACAGGCCCAACCAACCATGGAGGCTTGTGTAGAGAGAGCTC 789
OY 139 ---AspThrTTPApRyIyIySerNIeIyAlaMeIcThr---IyPhe----- 151
Db 790 TGTTCACATGGCTCGAAATATAGAGATTTTAAACAAAATTCACAGAGCTGTACTT 845
OY 152 -----AlaGIuGIuGIuAaNIaIaArGIaArSerPheGIuAaThr 164

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Db      949 TTATTTGGCCCAAGCGCTGATACCA-----GAACCTCGATGATGCTACTG 996
Qy      193 HisGlySerGlyIleGlyLeuSerAlaLeuAlaArgArgIleValLeuCySTrpAla 212
Db      997 CAGGGGCGCTGGTAATGGAGATCACTGGCCAGGCAAGTGAAGAAAGACCTGGGG 1056
Qy      213 GlnGlyLeuLeuTyrglnGlnGlyMetPheSerTyrrValPhePheLeuProValArgGluMet 232
Db      1057 AGAGCGCGCTGTATGGGACCGCTTCAGCATGTCTTCACTCACTGCAGAGAGCTG 1116
Qy      233 GlnArgLysLysGlnSerSerValThrGlnPheIleSerArgGlnTrpProAparSerGln 252
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Qy      410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCyLeuAsn 429
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Db      1744 AAAAAGACCTTTTCACTCAAGATGACTCAAGAAAGCAATGGTTAGTGGGCTCATC 1803
Qy      470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAparSerHisGlyGlu 485
Db      1804 TCCACCTTCTTGAAGATGGTATTTCTCAAGAGCACCCATCTCTGAGC----- 1854
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Qy      506 LeuGlnGlyLeuGlu-----IleGlnProAlaLeuCyProLeuTyrrValGlnLysThr 523
Db      1909 TTGAGGATGAGAAAGGAGAGGTAAACATTTATATTCATCACTAATTTGGAAAGAGCG 1968
Qy      524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
Db      1969 CTAGAGCA-----TATGAATATACATGCGCTGTGTTGGGCGATCA 2007
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Qy      561 LeuGlyCyProValProLeuGlyValLysGlnLysLeuHisIleTrpValSerLeuLeu 580
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Qy      581 Gly-----GlnGlnProAsnAlaThrThrProGlnAparThrLeuAparPheHisCy 598
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QY 1014 LeuThrSerAspCyAsnGluAlaLeuSerLeuAlaLeuSerCyAsnArg----- 1030
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QY 1038 -----ValGlnAsnAsnPheSerProLysGlyMet--MetLys 1049
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Db 3367 GACATCAA-----GGCTGAGCTGGAGCTGTGA--AGCTGTGACCTCTCCACCTT 3417
QY 1228 Ys-----ProThrValLeuMetThrThrAlaValCysProGluHisTrpGluArgLeuG 1246
Db 3418 GTGGCTCTCCAGAGGG--GCCATGTGACATCCCTGT--TCCAAATGGCCCACTTTAA 3473
QY 1246 LysSerArgGly-----TrpCyLeuAsnSerAlaAspArgHisSerGlyValSerTrpS 1264
Db 3474 AGAGAGGGGATGCTCTG-----AGAAAGCCAGCCAGGTGGA 3512
QY 1264 er 1264
Db 3513 GC 3514

RESULT 4
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT FILING DATE: 1999-09-01
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4272)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-388-221B-11

Alignment Scores:
Pred. No.: 2,646-90 Length: 4466
Score: 948.00 Matches: 360
Percent Similarity: 38.47% Conservative: 207
Best Local Similarity: 24.42% Mismatches: 529
Query Match: 13.40% Indels: 380
DB: 4 Gaps: 46

US-10-066-521-6 (1-1344) x US-09-388-221B-11 (1-4466)
QY 11 SerTrpGlyLeuGlnTrpCyLeuTrpGlu--LeuAspLysGluGlnPheGlnThrPhe 29
Db 13 GCTTGGGCGCGCTGAGCTGTACTTCTGAGATCTGTAAGAAGAGAGCTGAAGAGATTC 72
QY 30 LysGluLeuLeuLysLysSer--SerGluSerThrThrCysSerIleProGlnPhe 48
Db 73 CAGCTTCTGCTCGCAATTAAGCGCACTCCAGAGCTTCTGGGTGAGACACCTCGTCAG 132
QY 49 GluIleGluAsnAlaAsnValGluCyLeuAlaLeuLeuLeuHisGlyTrpTrpGlyVala 68
Db 133 CCAGAGAAAGAGAGTGCATGAGAGTGGCTCTGACTGTGTGCTGAG--TATGGGAG 189
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
Db 190 CAGCGGCTCTGAGACTGACCTCATACCTGGAGAGCATGGGGCTGAGATCACTGTGC 249
QY 89 GlnLysAlaArgAspArg----- 94
Db 250 GCCCAAGCCAGAAAGGGGAGGCGCACTTCCCTCATTTCCCTACAGCCCAAGTGAACCC 309
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94 ----- 94
Qy 310 CACCTGGGGTCTCCAGCCAAACCACCTTCACCGGAGTGAATGCCCTGGATCATGAA 369
Db 94 ----- 94
Qy 370 TTGCGGGGGGTGACCCAGAGGCTCAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429
Qy 95 -----MetLysLysIleSerGlnAlaMet----- 102
Db 430 TCTGAGCGCCGCTGAGAGAAATCTGCTCCTCCTCTACCAAGCTTTCAGAGCTCC 489
Qy 102 ----- 102
Db 490 CCAGACCATGAGTCTCCAGCCAGAGAGTCAACCCCAATCCACAGCAGAGTCTG 549
Qy 103 -----GluGlnGluGlyAla--- 107
Db 550 GGGAGCTGGGGATCCCACTCAGCCCAAGCTTACCCAGAGAGAGAGGCTCTGG 609
Qy 108 -----ThrAlaAlaGluThrGlu 114
Db 610 ACCCAATGCTCTGATGAACGTCAAGAAATTACTACAGAAATCAGAGAAAGAG 669
Qy 115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGln 134
Db 670 AGAGAGAAATCAGAGAAAGAGAGGCCCCCATGGGAGCGGTGATGAAACCCCCACAG 729
Qy 135 GlyHisGlyGly----- 138
Db 730 GCGCAGACCAAGCCTACAGCCCAACCAAGCCATGGAGCCTTCTGTGAGAGAGCCTC 789
Qy 139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe----- 151
Db 790 TGTTCACATGCGCTGAGAAATGAGGATTTTAAACAAATTCACACAGCTGCTACTT 849
Qy 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
Db 850 CTACAAAGACTCAACCCAGAGCCAGATCCCTGTGTAAGAGAGC----- 897
Qy 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
Db 898 -----TGGCTGATTAATGTGAGAGAGATGAGACATTAATTAATGATCAGAGAC 948
Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValLeu 192
Db 949 TTATTGGCCCAAGGCTGGATACCA-----GAACCTCGCATGATCACTACTG 996
Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCyTrpAla 212
Db 997 CAGGGGCTGCTGGAATTTGGAGATGACACTGGCCAGGAGGTGAGAGAAAGCCCTGGGG 1056
Qy 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
Db 1057 AGAGGCGAGCTGTATGGGAGACCGCTTCAGCAGATGCTTCTTCACTTCAGCTGAGAGAGCTG 1116
Qy 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
Db 1117 GCCCAGTCCAAGGTGATGCTCGCTGAGCTCATCGGAAAGATGGGAGCCACTCGG 1176
Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPhe 272
Db 1177 GCTCCCAATTAAGAGATCTGTCTAGGCCAGAGCGGCTGCTTCACTTCCTGATGGGTGA 1236
Qy 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCyLysAspTrpAlaGlu 291
Db 1237 GATAGACCAAGATGGGTCTTTCAGAGAGCCGAGTTCTAGCTGTCTGCACTGAGCCAG 1296
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
Db 1297 CCACAGCGCGGGGATGACACTGCTGGGAGGTTTGTGGGAAACATATCTCCCGAGGCA 1356

Qy 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
Db 1357 TCTTCCGTGATCAGGGCTGGACCAAGCTCTGAGAAACATTCCTTCTTGGAGAG 1416
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGlu 351
Db 1417 GCAGTGGGGTGAAGGCTCTGGGGTCTCTGAGTCCAGAGAAAGAAATATTCTACAGA 1476
Qy 352 ArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
Db 1477 TATTTCACAGATGAAGCAAGCAATTAAGACCTTTAGGTTGGTCAATTAACAAAG 1536
Qy 372 LeuLeuAspGlnCyGlnValProAlaValGlySerLeuIleCyValAlaLeuGlnLeu 391
Db 1537 CTCTGGGCTGTGTCTGTGTCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1596
Qy 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409
Db 1597 CAGATGAAGCGGAAGAAACTCACTGACTTCCAGAGCACACAAACCTCTGTCTA 1656
Qy 410 HisAlaIlePheValPheHisGlnLeuThrProArgGlyValValArgArgCyLeuAsn 429
Db 1657 CATTACCTTGGCCAGGCTCTCAAGCTCAAGCATTTGGGA----- 1695
Qy 430 LeuGluGluArgValValLeuLysArgPheCyAspMetAlaValGluGlyValTrpAsn 449
Db 1696 -----CCCAAGCTCAGAGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1743
Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeu 469
Db 1744 AAAAAGACCTTTCACTCAGATGACCTCAGAAAGCATGGGTGAATGGGGCATCATC 1803
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCyGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCAACCCCACTCTGAGC----- 1854
Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCyValAlaLeuTyrTyrVal 505
Db 1855 -----TACAGCTTCATCACTCTGTTCCTCAAGAGTCTTGTGAGCAATGCTATGTC 1908
Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCyProLeuTyrValGluLysThr 523
Db 1909 TTGAGGATGAGAGGGGAGAGATTAACATCTTAATGATCATATGATTTGGAAAGAGCG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
Db 1969 CTAGAGCA-----TATGAATACATGGCTGTGTGGGGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACAGCTTCTTATGGGCTGTATAGTATGAGGGGAGAGAGATGAGAAATC 2067
Qy 561 LeuGlyCyProValProLeuGlyValLysGlnLysLeuLeuHisIleTrpValSerLeuLeu 580
Db 2068 TTTCACTGCGGCGGTCTCAGGGG-----AGAAACCTGAGAGAGTGGTCCCGCTCTG 2121
Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGluAspThrLeuAspAlaPheHisCy 598
Db 2122 CAGCTGCTGTGCGCCACAC-----TCTGTGAGTCCCTCGACCTG 2163
Qy 599 LeuPheGluThrGlnAspValGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db 2164 TTGTACGAGCTCGGAACAAACCTTCTGACACAGATGATGGCCATTTGGAAAGATG 2223
Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerPheCyLysGlnHisCy 638
Db 2224 GGCAATGTGTAGAAACAGACATGAGCTTTAGTGTGCACTTCTGATTAATTCAGC 2283
Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658
Db 2284 CGCCAGCGGAAGAGCTTCAAGCTG---ATTGAGGC-----AGCAGACACAGATCA 2331
Qy 659 GluAlaCyProValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678

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Db 2332 ACATGAGCCGCCACATGAGTGTCTGTTCAGTGGGTCCCAAGTCAAGAGCTTATGG 2391
Qy 679 GluapRheCySerMetLeuGlyThrHisProHisLeuArgGlnLeuAapRLeuGlySer 698
Db 2391 ----- 2391
Qy 699 SerLeuLeuThrGluArgAlaMetLysThrLeuCySalaLysLeuArgHisProThrCys 718
Db 2391 ----- 2391
Qy 719 LysLeuGlnThrLeuMetPheArgAspAlaGlnLeuThrProGluValGlnHisLeuThr 738
Db 2392 ----- 2403
Qy 739 ArgLeuValMetAlaAsnArgAsnLeuArgSerLeuAenLeuGlyGlyThrHisLeuLys 758
Db 2404 TCCGCTCCTCAAGGTCACCAAGAACCTGAAGAGCTGACCTTAAGTGAAGAACTGGTAAAGC 2463
Qy 759 GlnGluAapRValArgMetAlaCySgGlnAlaLeuLysHisProLysCySLeuLeuGlySer 778
Db 2464 CACTCTGAGTGAAGAGCTTGTAAAGACCTGAAGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 2523
Qy 779 LeuArgLeuAapRValArgMetAlaCySgGlnLeuThrHisAlaCySgGlnLeuLysHis 798
Db 2524 CTGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2583
Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuGlnAlaGlnLysValThrAapRLeuGly 818
Db 2584 AGAGCCCAACAGACCTGAGCCAGAGCTGAGCTTCAATGAGCTTCAATGAGCTTCAATGAG 2643
Qy 819 ValMetProLeuSerAapRAlaLeuArgValSerGlnCySalaLeuGlnLysLeuLysLeu 838
Db 2644 GCCAAACACCTTTCGCAAGAGCTGAGACAGCCGAGCTGCAAGCTTCAAGCTGCAAGCTG 2703
Qy 839 GlnAapRValArgMetAlaCySgGlnLeuThrHisAlaCySgGlnLeuLysHisValSer 858
Db 2704 GTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2763
Qy 859 ArgSerLeuThrHisLeuCySLeuSerAapRAsnLeuGlnLysValGlnLysLeuLysLeu 878
Db 2764 CCCAGCTTGAAGAGCTTGAAGCTGAGCTGAGCAAGAACCTGAGTACCTGTTGGGCTGAGCTG 2823
Qy 879 LeuCySArgSerMetArgLeuProHisValSerLeuGlnArgLeuMetLeuAapRLeuGln 898
Db 2824 CTCTGTGAGGGGCTCAGGCAATCTGCTGCTGCAATCATAGCTGCTGCTGCTGCTGCTGCTG 2883
Qy 899 HisLeuAapRThrAlaGlyCySgGlnPheLeuAlaLeuAlaLeuMetGlyAapRLeuTrp 917
Db 2884 ATGACCCCTTACTGAGGGC-----CTGGATACGGGAGAGATGATGATGATGATGATGATG 2934
Qy 918 -----LeuThrHisLeuSerLeu-----SerMetAapRProValGlnAapRAlaGly 932
Db 2935 TCACCTCAAGCGGCAAGACTGGATCAGAGAGGGGGCTTCCCATGTTGCTCAGGCTTAAT 2994
Qy 933 ValLysLeuLeu-----CySgGlnValMetArgGlnProSer 944
Db 2995 CTCAAACTCCTGAGCTGAGCAAGATCTTCCCAATGCTGAGTATGTCAGAGGAAAGCTCC 3054
Qy 945 CySHisLeuGlnAapRLeuGlnLeuVal-LysCys-----HisLeuThrAlaAlaCy 961
Db 3055 CCAAGAGTAAAGTACCGGTGAACCTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3114
Qy 961 CySgGlnSerLeuSerCySalaLysSerArgHisLeuLysSerLeuAapRLeu-- 980
Db 3115 CATACGAAGCTTGTGGGACTGACAGATGATCTTGTGGGGCTGTGAAGAAAGATGATGATG 3174
Qy 981 -----ThrAapRAlaLeuGlnLysAapRLeuGlnValAlaAlaLeu 993
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Qy 993 uCySgGln-----GlyLeuLysGlnLysAapRLeuVal 1004
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Db 3235 CTGTGCTCAGCCACAGAGCTTGGCTTCTGCTGTAAGGATGAGTACAGTACAGTATGGC 3294
Qy 1004 uThrArgLeuGlyLeuLysAlaCySgGlyLeuThrSerAapRValAlaLeuSerLe 1024
Db 3295 TTTGGTTCCTGAGAGTCAAGCACTGGCCCTGAGCTGCAAGCAATGAAGTGGCTGGTG 3354
Qy 1024 uAlaLeuSerCySalaAapRHisValLeuThrSerLeuAapRLeuValGlnAapRLeuSerP 1044
Db 3355 GCGCGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3402
Qy 1044 OlySgGlyMetMetLysLeuCySer-----AlaPheAlaCySProThrSerA 1060
Db 3403 GAATTCACCTCCCTCCCTCAATCTCCCTCCCAAGTGAAGTGAAGCTGCTGCTGCTGCTGCT 3462
Qy 1060 nLeuGlnLeuLeuLeu-----TrpLysTrpGlnTrpProValGlnLeuArgLysLe 1078
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Qy 1078 uLeuGlnGlnValGlnLeuLeuLysProArgValValLysAapRLeuSerTrpHisSerP 1098
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Qy 1098 eAapRValAapRArgHisLysLysLysLeuThrPheArgLeuProGluSerArgAlaTr 1118
Db 3576 CGCCAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3615
Qy 1118 ProCySAlaLeuLeuTrpGlnLysMetAapRProGlnGln-----LysLysArgValSerLeu 1137
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Qy 1157 nGlyGlySerGlnArgValAapRAsnValGlnGlnSerProGlnProMetAla----- 1175
Db 3705 TGATGAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3764
Qy 1176 -----GlyThrGlnHis-----LysGln 1181
Db 3765 GAATTTGGTTCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3824
Qy 1181 nAapRLeuMet-----LeuSerValGlyTrpSerGln 1191
Db 3825 GTTGAAATTTGCTCAAGAGCCCTGAGAAATTCACAGCTTCCAAATTCATGCTGCTG 3884
Qy 1191 yAlaTrpSerGlnThrAlaGlnLeuGlnGlyLeuGlySerAapRLeuAapRHisAapRHis 1211
Db 3885 GCAGATGAAGAAACCATTAACCTGAG-----ATTACTGAAGAAAGACA 3929
Qy 1211 sGlyGlyMetAlaTrpSerLeuGlyArgGlnLeuSerSerArgGlyLeuCyS----- 1228
Db 3930 TGGGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3988
Qy 1229 -----ProThrValLeuMetThrThrAlaValCySProGly 1240
Db 3989 CAGCCCTCCTCTTCTCAGAGTCAAGCTTGTGAAGGA 4028
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RESULT 5
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent NO. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388, 221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA


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Db 3732 CGAAGATATTAAGTTCACCTTGACCTTGCCCGACGAC----- 3771
Qy 1147 eAllylseryleuylalaThrAlaanglylserglnargValaAspValaGl 1167
Db 3772 -----GCCTTGCTAACAAAGCGATAGATGATGAAGATCGCTTCATGCTGCG 3824
Qy 1167 uGlnserProGlnProMetAla-----GlyThrGlnHis----- 1179
Db 3825 CCGCAGACTTCGCCCCCAATGGAACCCCTGAACCTTGATTCATATATGTCTAA 3864
Qy 1180 -----LysGlnAspLysMet----- 1184
Db 3885 TTCTGCTAACCTGAAGATATCCCAAGAGATGTAATTCCTACAGAGCCCTGAGA 3944
Qy 1185 -----LeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGl 1201
Db 3945 AATTCAGCACTTCTCAAAATTCATATGCTGGCGATGAAAGAACCATTCAGAG-- 4002
Qy 1201 yLeuGlySerAsnSerAlaAspHisGlyGlyMetAlaTrpSerLeuGlyArgG 1221
Db 4003 -----ATTACTGAAAAAGACATGGAGCTTGCTGGGATCTGA-GGTGA 4048
Qy 1221 uLeuSerSerArgGlyLeuGlyS-----ProThrValLeuMetThrThrAla 1237
Db 4049 AGCCAGTGATCTCCAGCTTGAGCTGCATCAGCCCTCTCTTCAGGTGACGCT 4108
Qy 1237 lCyPrGly 1240
Db 4109 TTGTGAAGA 4118

RESULT 6
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-910-731-3

Alignment Scores:
Pred. No.: 4.28e-57 Length: 1374
Score: 630.50 Matches: 151
Percent Similarity: 51.38% Conservative: 73
Best Local Similarity: 34.63% Mismatches: 205
Query Match: 8.91% Indels: 9
DB: 2 Gaps: 3

US-10-066-521-6 (1-1344) x US-08-910-731-3 (1-1374)
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Qy 671 LysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHis 690
Db 97 TGTGGCTTACTAGTGGGCGGTGCAAGACATCAGAGTGGATGAGTCCAGGCCAACTCTCC 156
Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLeuThrLeuGly 710
Db 157 CTGACAGAGCTCAGCTATGACCAATGATGAGTGGGTATGCTGGGTGGTGGTCTG 216
Qy 711 AlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAspHisGlnIle 730
Db 217 CAGGCTCTGAGAAATCCCATTTGATGATCCAGAAAGCTGAGACCTTCAGAACTGACGCTTG 276
Qy 731 Thr---ProGlyValGlnIleLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSer 749
Db 277 AGGAGAGCTGGCTGGGGGCTGCTGCTGATGATGCTGCTGCTTGTCTAACCTGCGTGA 336
Qy 750 LeuAsnLeuGlyIleThrHisLeuLysGluGlnLysArgValaArgMetAlaCysGluAlaLeu 769
Db 337 CTACATCTCATGACAAACCTCTGGGGGATGAAAGCCGATGAGCTGTGTGAAGGATC 396
Qy 770 LysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysGlyLeuThrHisAla 789
Db 397 CGGAGCCCCAGTCCGCTGAGAAAGCTTCACTGGAATCTGTAACCTCAGACGCTACC 456
Qy 790 CysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeu 809
Db 457 AGCTCGAGCCCTGGGCTCAGTCTCAGAGTGAACCTTAAAGACCTGATATG 516
Qy 810 AlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSer 829
Db 517 AGCAACATGACTTCATGAGCGGTATCCACTCTGTGCCAGGCTGAAGATTC 576
Qy 830 GlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGln 849
Db 577 GCTGTCACTGAGTCACTCAAACTGGAAGCTGTGTATCACTCAGCCCACTGCAAG 636
Qy 850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsn 869
Db 637 GATCTGTGATGTGTGGCTCCAAAGCTCAGTGAAGACTGAGTCTGGCGAAC 696
Qy 870 SerLeuGlyAsnGluGlyValaAsnLeuLeuCysArgSerMetCysLeuProHisCysSer 889
Db 697 AAGCTGGCAACAGAGATTCAGACATGTGCTCAGAGCTGTCTTCCAGCTGACG 756
Qy 890 LeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAla 909
Db 757 CTGAGAGACTGTGGCTCTGGAGCTGATGTCTAGTGAAGAGCTGAGAAAGACTGTGC 816

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Qy 910 LeuAlaLeuMetGlyAsnSerThrLeuThrHisLeuSerLeuSerMetAsnProValGlu 929
Db 817 CGTGCCTCAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 876
Qy 930 AspAsnGlyValIleValLeuLeuValMetArgIleProSerCysHisLeuGlnAsp 949
Db 877 GATGAGGCTGCCCAAGCTCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
Qy 950 LeuGluLeuValIleCysHisLeuThrAlaIleCysCysGluSerLeuSerCysValIle 969
Db 937 CTGGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
Qy 970 SerArgSerArgHisLeuLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeu 989
Db 997 ACCAAAGACAGTCTCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
Qy 990 ValAlaAlaLeuValCysGluGlyLeuValCysGluValIleValLeuThrArgGlu 1009
Db 1057 GTCCGAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1116
Qy 1010 LysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCys 1029
Db 1117 GAGAGCTGTGATGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1176
Qy 1030 ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProIleGlyMetMetI 1049
Db 1177 CGCAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
Qy 1050 LeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu----- 1066
Db 1237 CTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1296
Qy 1067 ---TTPySTrGlnTrpProValGlnIleArgIleGlyLeuGluGlu 1081
Db 1297 TACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1344

RESULT 8
US-08-910-731-1
Sequence 1, Application US/08910731
Patent No. 5932440
GENERAL INFORMATION:
APPLICANT: CHATTERJEE, DEB K.
APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893

```

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REFERENCE/DOCKET NUMBER: 0942.3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-910-731-1

Alignment Scores:
Pred. No.: 4.49e-56 Length: 1371
Score: 621.00 Matches: 151
Percent Similarity: 50.11% Conservative: 86
Best Local Similarity: 31.92% Mismatches: 210
Query Match: 8.788 Indels: 26
Gaps: 5

US-10-066-521-6 (1-1344) x US-08-910-731-1 (1-1371)
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Db 4 AACCTGAGATAT-----CATTCGAGACAGCTTGAAGAGAGAGAGAGAGAGAGAGAG 39
Qy 645 ArgValAspValIleGlyIlePheProArgAspGluSerAlaGluAlaCysProValVal 664
Db 40 CGG-----TGAGAGAGCTCTGCGCTGCTC 66
Qy 665 ProLeuTrp-----MetArgAspIleThrLeuIleGluGlnIleTrpGluAsp 680
Db 67 CAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
Qy 681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db 127 ATCGGTTGTGCTCTCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
Qy 701 LeuThrGluArgAlaMetIleThrLeuCysAlaIleValAsnHisProThrCysValIle 720
Db 187 CTGGCGATGCCCGGAGTGCACCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
Qy 721 GlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeuTrpArg 739
Db 247 CAGAGAGTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuValGlu 759
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Qy 760 GluAspValArgMetAlaCysGluAlaLeuIleValHisIleProIleCysLeuLeuGlySer 779
Db 367 GCCGCGCTGCGAGTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
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Db 427 CAGTTGAGAGTACGCGCGCTTACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
Qy 800 ThrSerProSerLeuValSerLeuSerLeuAlaGluValIleValIleValIleVal 819
Db 487 GCCAGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
Qy 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnIleValIleValIle 839
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Cy 880 CysArgSerMetArgLeuProHisCySerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db 727 TGGCCCGGGCTCTTGAGCCCGGCTCCCGCTCAAGACCTGTGGCTCTGGAGAGTAC 786
Cy 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
Db 787 ATCAGCCGCACTGGCTGAGAGAGACTTGGCCCTGTCTCCAGGCGCAAGAACCTGAG 846
Cy 920 HisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValLeuLeuCyGlyVal 939
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Cy 940 MetArgGluProSerCysHisLeuGlnAspLeuGluValLeuValCysHisLeuThrAla 959
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Cy 960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLeuSerLeuAsp 979
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Cy 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
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Cy 1040 AsnAsnPheSerProGlyGlyMetMetLeuLeuCySerAlaPheAlaCysProThrSer 1059
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Cy 1060 AsnLeuGlnIleGlyLeuTrpIleTrpGlnTrpProValGlnIleArgLysLeuLeu 1079
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/ FILING DATE: 04-FEB-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/024,057
/ FILING DATE: 16-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ESKOMD, ROBERT W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0942.3440002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1371 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1368
/ US-08-795-395-1
/
Alignment Scores:
Pred. No.: 4,49e-56 Length: 1371
Score: 621.00 Matches: 151
Percent Similarity: 50.11% Conservative: 86
Best Local Similarity: 31.92% Mismatches: 210
Query Match: 8.78% Indels: 26
DB: Gaps: 5
US-10-066-521-6 (1-1344) x US-08-795-395-1 (1-1371)
Cy 625 AsnLeuAspLeuIleAlaSerSerPheCysLeuGlnIleCysProTrpLeuArgLysIle 644
Db 4 AACCTGCAATAT-----CATTCGAGCAGCACTGAGGAGCGCC 39
Cy 645 ArgValAspValLysGlyIlePheProArgAspLysSerAlaGluAlaCysProValVal 664
Db 40 CGG-----TGCAGAGAGCTCTCCGCTGCTC 66
Cy 665 ProLeuTrp-----MetArgAspLysThrLeuIleGlnGlnTrpGlnAsp 680
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Cy 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTrpLeuLysIleSerGlnIleLeuThr 799
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Qy 1060 AaLeuGlnIleLeuGlyLeuThraIleThryTrpGlnIleValGlnIleArgLeuLeu 1079
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Qy 1080 GlnGlnValGlnLeuLeuLeuPro-----ArgValAla 1090
Db 1327 CAGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942,3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-910-731-7

Alignment Scores:
Pred. No.: 4,18e-55 Length: 1371
Score: 612.00 Matches: 152
Best Local Similarity: 49.26% Conservative: 81
Query Match: 32.14% Mismatch: 214
DB: 8.65% Indels: 26
Gaps: 5

US-10-066-521-6 (1-1344) x US-08-910-731-7 (1-1371)
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Qy 665 ProLeuTrp-----MetAargAapLeuThraIleGlnIleGlnIleTrpGlnAap 680
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Db 127 ATCGATTCTGCCCTCCGCGGCGCAACCCCTGACCGAGCTGTGCTGCTGCGACCAAGAG 186
Qy 701 LeuThraGlnAargAlaMetLeuThraCysValAlaLeuAargHisProThraCysValIle 720
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Qy 721 GlnThraMetPheAargAanAlaGlnIleThra--ProGlyValGlnHisLeuTrpAarg 739
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Qy 740 IleValMetAlaAanAargAanLeuAargSerLeuAanGlnIleGlnIleValLeuGln 759
Db 307 ACGCTGCGCTCCCTGCGCCAGCCGCTGCGAGAGCTGATCTCAGAGCAACCCAGCTGGGAGC 366
Qy 760 GlnAapValAapMetAlaCysGlnAlaLeuLeuHisProLyGlyLeuLeuGlnSerLeu 779

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Qy 798 LeuThrHisSerProSerLeuLysSerLeuAlaGlyAlaAspValThrAspGln 817
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Qy 818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 837
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Qy 858 AsnArgSerLeuThrHisLeuLysSerAsnAsnSerLeuGlyAsnGluGlyValAsn 877
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Qy 1038 ValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysAsp 1057
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Db 1336 CCGGTGAGGCGCTGAGAGAGAGCAAGCATCCCTGAGAGGTTCATC 1380

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RESULT 12
 US-09-799-451-870
 ; Sequence 870, Application US/09799451
 ; Patent No. 6783969

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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qiang A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yundong
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc FL_genes Version 2.0
SEQ ID NO 870
LENGTH: 3156
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (478)..(2565)
US-09-799-451-870

Alignment Scores:
Pred. No.: 3,04e-32 Length: 3156
Score: 406.00 Matches: 286
Percent Similarity: 35.04% Conservative: 152
Best Local Similarity: 22.88% Mismatches: 420
Query Match: 5.74% Indels: 392
DB: 4 Gaps: 55

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Db 1 ATGAGCTACTTTCGCGCACCCGAGAGAGCTGCGCTGAGATCAAGCCAGGCGG 60
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Db 61 CTCCTCCCACTG---GCCCTTCTCACTCTTTAAACCGGATGCTGTGGCGCGGCTG 117
Qy 188 ArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIle 207
Db 118 CAGACAGTGTGTCTGTATGAGACAGTGGGACAGGAGCAAGACAGCTGTGCGCAAGT 177
Qy 208 ValLeuCysTrpAlaGlnGlyLysLeuTrpGlnGlyMetPheSerTrpValPhePheLeu 227
Db 178 GTTCTGAGCTGTGTATGCGGCGCTGCGG-----GCATTGAGCTGCTCATC 225
Qy 228 Pro-----ValArgLysMetGlnArgLysValGlyLysSerValThrGlu 242
Db 226 CCTCTTCTCTGTGAGAGAGTGTATCCGTGGCGGT---GCCAGGCTTCATGTGCCAA 282
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Db 283 CTGTGCGCCAGCGCTAC-----ACGCTCTGAAGAGAGTTCGCTGCTCATATG 330
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Db 331 GCTGCTGCTGTGTGCCACCTCTCTTGTGTCTCATATGCTTATAGACAT----- 378

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OY		475	Met-----AsnlleuleuProAprSerNHsCyeglun---	486
Dd		1042	ATCTTCGTCGGGATGCCCTGATGGTTTTCTGGGCCCA-----TGTGTGAGCCA	1092
OY		487	-----TyrTyrrThrPhePheNHsleuSerLeuGlnmarPheCyvalAlaleu	502
Dd		1093	GGGCGTGCAGGACCTTGATGTATCAACCTGCCGACATGCAAGAAATACCTGGCTGCCTC	1152
OY		503	TyrTyrrValleuGlnGlyleuGlnlunleuGlnProAlaleuCyvProleuTyrrValGluLyS	522
Dd		1153	TACATGTAGCTG---GGTTG-----	1170
OY		523	ThrIyVArGrSerMetGluyleuLySGlnAlaglyPheNHsIleNHsSerleuTrpMetLyS	542
Dd		1171	-----CCCAAGACACACCTTGCAAAAGGTGGCAGAAAGTGGTAG-	1212
OY		543	ArgPheleuPheGlyleuValSerGlnmarValAlargArGrProleuGlnlunleuGlu	562
Dd		1213	-----CTCGTGGGGCGTGTGGAGGACCTC-----	1235
OY		563	CysProValProleuGlyValLySGlnlyleuLeuNHsITrpValSerleuGluGln	582
Dd		1240	---AGCTTGGTACTGGGACATCAAGGCCACCTGCTG-----	1272
OY		583	GlnProAsnalatThr-Thr-ProGlyuarThrThreularAlarhenIsCyvleuPheGluThr	602

Db	1273	-----CCTGCGGGCTCTGCTCTGCTTCAACCTGATCAAGGTC	131
Qy	603	GLnAspYsGIuPhVaLaIrgLeuAlaLeuAnSerPheGlnGluValTrrPleuProIle	622
Db	1315	GTTCACAGAGGTTTGGCGCATG-----GAG	1341
Qy	623	AsnGlnAnLeuAspLeuIleAlaSerSerPheCySLeuGln-----	636
Db	1342	GSTAAAGCCCGGAGGCGGTGGCTTCAGGCCATGTGTGTGGAGATGTTTCAGAGGAGNC	1401
Qy	637	-----HisCySProTYrLeuAlxgYsIleArgValAspValYsGlyIlePhe-----	652
Db	1402	TACTACAAACGATGATGTTCTGACACGAGATGGAGCCGCACTATCTGGGGGTGGAGGACCC	1461
Qy	653	-----ProArgAspGluSerAlaGluValAAspProValAlaPro	665
Db	1462	CGGGCCCAACCAAGATGAGCCCCCTGAGATGAAGCTTCGAG-----CTCTTCCC	1511
Qy	666	LeuTrrMetArgAspYsThrLeuIleGluGluGlnTrrGluAspPheCySerMetLeu	685
Db	1513	ATGTTCAATGGGG-----GGGCTTCTC	1531
Qy	666	GlyThrHrIAspProHrIAspLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla	705
Db	1534	TCTGCCCAACAACGAGCTGTGCTGAGCTGAGCTTGAC-----	1561
Qy	706	MethYsThrLeuCySAlaYsLeuArgHrIAspThrCySlySileGlnThrLeu---Met	724
Db	1570	-----TCCCATCAAGACCTGATGTC	1591
Qy	725	PheArgAsnAlaGln---IleThrProGluValGlnHrIAspTrrArgIleValMetAla	743
Db	1594	CTGAGAGATGCCAGGCCATCAAGAAAGAGCTGGGCAAGCTGGCGGCGAGGTGCTGCC	1653
Qy	744	AsnArgAsnLeuAspSerLeuAnLeuGlyGlyThrHrIAspLeuGluGlnAspValArg	763
Db	1654	CCATCAGAGCTC-----CTTGACCACTCTTCTTCCACTAGATGTCAGAAACAGCGC	1701
Qy	764	MetAlaCySgIuAlaLeuYsHrIAspProYsCySLeuGluSerLeuArgLeuAspCyS	783
Db	1708	TTCCTCCGTGAGGCTCAGC-----	1722
Qy	784	CysgIyLeuThrHrIAsaCySlyrLeuYsIleSerGlnIleLeuThrThrSerProSer	803
Db	1729	-----TCC	1731
Qy	804	LeuYsSerLeuSerLeuAlaGlyAsnYsValThrAspGlnGlyValMetProLeuSer	823
Db	1732	CTGCCTCAGCTCAACCTTGAGGAGTGTGCGCATGACACCACTCAAGTCAAGTGTGTGGCA	1791
Qy	824	AspAlaLeuArgValSerGlnCySAlaLeuGlnYsLeuIleLeuGluAspCySgIyIle	843
Db	1792	GCTGTGCTGGGACGGAGGAGGATGCTCTGTGATGAGGAACTTGCGCTCTGCCAGCTA	1851
Qy	844	ThrAlaThrGlyCySgInSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHrIAs	863
Db	1852	GATCCTGTGGGCTGGCAGCATCTCGCTGTCTTCCTGCGCGGCCGGAGAGTGGGC---	1901
Qy	864	LeuCySLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCyArgSerMet	883
Db	1909	-----TGCACACTCAACAGGCTGGGCTCTGAGGCC-----TGCAGAGCACTTC	1951
Qy	884	Arg-----LeuProHrIAs-----CysSerLeuGlnArgLeuMetLeuAnGlnCySHis	899
Db	1951	CGAGACTGTGTGCTGCATGACCAAGTCCAAATTACACATGCGGCTGTGCAACAAACCG	2011
Qy	900	LeuAspThrAlaGlyCySgIyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrrPleuThr	919
Db	2011	CTGACGAGAGGAGAGTCTTGGCGGTGATTATGAGAGGGGCTGGCAGAAACCTCACTGACG	2071
Qy	920	HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValYsLeuLeuCySgIuVal	939

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Db      2071 CACCTGTCCTGTCGACACAGCGCCCTGGGAGCAAGGCGCTGAGACTG----- 2118
Qy      940 MetArgGluProSerCySHLeuGlnAspLeuGluLeuValLysCySHLeuThrAla 959
Db      2118 ----- 2118
Qy      960 AlaCySGluSerLeuSerCyValIleSerArgSerArgHISLeuLysSerLeuAsp 979
Db      2119 -----CTGGCTGCCAGCTGAGACCGGACACCGGACGCTGACAGAGCTGAGAC 2163
Qy      980 LeuThrAspAlaLeuGlyAspGlyGlyValAlaAlaLeuCySGluGlyLeuGln 999
Db      2164 GTGGCGTACAAAGCTGTGCTGTGACACAGCGCGCCCTGCGCCGACAGCTGCCGGGAG 2223
Qy      1000 LysAsnSer----- 1002
Db      2224 CACCTTCCCTGGAACCTGACACCTTAATTCAATGAGCTGAGCTCAGAGCGCGCCAG 2283
Qy      1003 ValLeuThrArgLeuGlyLeuLysAlaCySGly-----LeuThr 1015
Db      2284 GTCTTGGAGAGACTGGGGGGGCTGCTGAAAGTGTGCCGGGTGTGTGTCTGACAGCA 2343
Qy      1016 SerAspCySGly-----GluAlaLeuSerLeuAlaLeuSer-----CyAsnArgHISLeu 1032
Db      2344 GAGGGAGCGCGGTGTGCAAAATACCTGATCTGATGATCTGAAAGTCCAGCGGAACCTC 2403
Qy      1033 ThrSerLeuAsn-----LeuValGlnAsnAspHe 1042
Db      2404 AATGACTGGAGATCGGGCCCGGTTCAAGCAGACCTTGAGCTCTAATCGGAGATCTGAA 2463
Qy      1043 SerProLysGlyMetMetLysLeuCySerSerAlaPheAlaCySGlyProThrSerAsnLeuGln 1062
Db      2464 GATAGCCGGGT-----GCCACCTTAATCTTGGCGGAGAGCCCGAG 2505
Qy      1063 IleIleGlyLeuTrpLysTrpGlnTrpValGlnIleArgLysLeuLeuGluGlnVal 1082
Db      2506 CTGCTG-----CGAGTGGAGGCGGAGCTCAAGGCGCTCTGAGCAGACTG 2550
Qy      1083 GlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlnAspAsp 1102
Db      2551 -----GMAAGCTCTGAGAGCTGAGACCTGGCGGC 2580
Qy      1103 ArgHis-----LysIleGlyLeu-ThrPheArgLeuProGluSerArgAlaTr 1118
Db      2581 AGGCACTCAAGTATGTACACCTGCGCTTAACCTTTCCCTC----- 2623
Qy      1118 pProCyAlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAl 1138
Db      2624 -----TGCGCTCTGCTGCTGACGCTCCCTTAAGAAAGATCTTCAAGGCTGAGAGC 2679
Qy      1138 ArgLysAspPhe-LysSerSerThrArgPheAlaLysSerLeuCyLeuAlaThrAlaAsn 1158
Db      2680 AGAGGAATGGGCATATGAGCCAGCTGCTCTAGGGCATGTTTGACAGAGACTGAGT 2739
Qy      1158 LysGluSerGlnValAlaAspAsnValGluGln-SerSerProGlnProMetAlaGlyThr 1177
Db      2740 CTGGAATCTCCAAAGTAAAGATGTAATCAATCAATCTGGGCTTGGAGATG----- 2790
Qy      1178 GluHis-----LysGlnAspLysMetLeuSerValGlyTyrSer 1190
Db      2791 GAACATGCTCTCTCCATTCATTCAGCTAGAGAGCAAGCAAGCATTTGGCATTTGAGCGCAG 2850
Qy      1191 GlyAlaTrp-SerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaAsp----- 1208
Db      2851 AGTCCCTGAAAGCACCACTTCAACCTTCCCTCTCAAAAGAGCCTTGATTTG 2910
Qy      1209 -----HisAspHisGly-----GlyMetAl 1215
Db      2911 TGTCAACCAAGGGCTCACATTTATGTCTGCCATGCCAGGGGTGTGCCCATCCAGATTTG 2970
Qy      1215 ATPSerLeuGlyArgGluLeuSerSerArgLysLeuCyAspProThrValLeuMetThrTh 1235
Db      2971 TTGAGAGTT-----CCCTCTGCTGCTTATGTCTACCTGTGAGC 3009

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Qy      1235 rAlaValCySGlyProGlyHisTrp 1242
Db      3010 ACCGAGGATGCCCTTCACATTTGG 3031

RESULT 13
US-09-245-281-42
Sequence 42, Application US/09245281
Patent No. 6369196
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 4141
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (261) ... (3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 3,63e-29 Length: 4141
Score: 379.50 Matches: 253
Percent Similarity: 37.01% Conservative: 150
Best Local Similarity: 23.23% Mismatches: 416
Query Match: 5.36% Indels: 273
Gaps: 46

US-10-066-521-6 (1-1344) x US-09-245-281-42 (1-4141)
Qy      6 SerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGluLeuAspLysGluGln 25
Db      451 AGCTGACAGAGCTCGAAAGATCTTAACCTGAGTGC----- 486
Qy      26 PheGlnThrPheLysGluLeuLysLysLysSerSerGluSerTrpThrCysSerIle 45
Db      487 -----AAGCAAGAGCGAGAGCGTGTGAGTTCTTCTCTACAGCTGCGCAG- 533
Qy      46 ProGlnPheGluIleGluAsnAlaAsnValGluCyLeuAlaLeuLeuHisGluTrp 65
Db      534 -----CAGCTGAGAGATGCTTACGTGAC--CTCAGGCTG----- 566
Qy      66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85
Db      567 -----TGCTCTCAAAATTTGCTTCTCCCTCCAGCTCATTTGG 608
Qy      86 ThrLeuSerGlyValAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlu 105
Db      609 ACCAAACTATTCGCATATCTGACCCAGTAAGCAGATATCCCAACAGCTGCGACACCA 668
Qy      106 GlyAlaThrAlaAlaGluThrGluGluGluGluLysSerGlnAlaMetGluGluGlu 125
Db      668 ----- 668
Qy      126 AlaThrAlaAlaGluThrGluGluGluGlyHisGlyGlyAspThrTrpAspTyrLysSer 145
Db      669 -----CTGGCGCGCGAC-----TCC 683
Qy      146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla 165

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Db 684 AAGTTCATGCTGTCTACGCCGAGAGAGACCTG-----CTGCTGGAGAGACC--- 734
 Qy 166 A1aAspTrpProGluMetGlnThrLeuAlaGly-----AlaPheAspSerAspArgTrp 183
 Db 735 -----TATATGACACACTATGGGGCTGGTAGGGCTTCAACAATGAAGAAACCTG 782
 Qy 184 GlyPhe-----Arg 186
 Db 783 GGCAGCCTAGAGAGCCTGATATGCTGCTGAGACCAAGTACGGGGCTCTGACAGACAT 842
 Qy 187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 206
 Db 843 GCGGAGACTGTCTTCCTGCTTGGGAGACCGGAGAGGAGTCAATGCTCTGCTGAGAG 902
 Qy 207 I1eValLeuCyvTrpAlaGlnGlyLysLeuTyrrGlnGlyMetPheSerTyrrValPhePhe 226
 Db 903 TTGCAAGCCTCTGGGGCTGACAGGAGGTTG---ACCTCACAAGCAATTTCTTCTTCAC 959
 Qy 227 LeuProValArgGluMetGlnArgLysLysGluSer-----SerValThrGluPhe 243
 Db 960 TTCGCTGCGCCATGTTCACTGCTTCAAGGAGACGACATGCTGACGTCTGACAGACTG 1019
 Qy 244 I1eSerArgLysTrp-----ProAspSerGlnAlaProValThrGluIleMet 259
 Db 1020 CTCTTCAAGCAATTTCTGCTACCCGAGACGAGACCCCGAGAGGTTCTCTTCTTGTG 1079
 Qy 260 SerArgProGluArgLysLeuPheIleIleAspGlyPheAspArgLysSer----- 277
 Db 1080 CGCTTCCCAACACAGCGCTTTCACCTTTTGAACGGCTCGATAGACTGACATCTAC 1139
 Qy 278 ValLeuAsnAspThrLysLeuCyvLysAspTrpAlaGlnLysGlnProPhePheThr 297
 Db 1140 GACCTGAGCCGCGTCCGATAGCTGCTGCCCTGG---GAGCCGGCTCACTCTGTGTC 1196
 Qy 298 LeuIleAspSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
 Db 1197 CTGCTGCTAACCTCTCAAGTGGAGAGGCTGCTCAAGGCTCGGCAAAATTTCTCACTGCT 1256
 Qy 318 Arg-----AspValGlyThrGluLysLeuLysSerGlnValValSerProArgTyr 334
 Db 1257 CGCACAGCGCTGAGAGTCCCCCGCACAGTCTTGGCGCAAAAGCTG----- 1301
 Qy 335 LeuLeuValArgGlyLysSerGlyLysGlnArgIleHisLeu----- 348
 Db 1302 ---CTGCTCGGGGCTTCTCCCAAGT-----CACCTGCCGCTTATGCCGCGG 1349
 Qy 349 ---LeuLeuGluArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
 Db 1350 ATGTTCCCGGAGCGACAGCGCAGAGAGCATCTG-----CTGCACAGCTGGAT 1397
 Qy 368 AsnAsnArgGluLeuLeuAspGlnCyvSerGlnValProAlaValGlySerLeuIleCyvVal 387
 Db 1398 GCGAAGCCCAACCTCTGACGCTGTGGGGGTGCGCTTCTGTGATATATCTTCGCT 1457
 Qy 388 AlaLeuGln---LeuGlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeu 406
 Db 1458 TGTTCACGACATTCACAGAGCGTCTTGAAGGGCTCTCTTCACAGTTCCGCACTGCT 1517
 Qy 407 ThrGlyLeuHisAlaAlaPheVal-----PheHisGlnLeuThrPro 420
 Db 1518 GTGACCTGACCGATGCTTCTGCTGTGTGCTACGTAGGTGATCTGAAAGCCGCGACGCC 1577
 Qy 421 ArgGlyValValArgArgCyvLeuAsnLeuGlnGluArgValVal----- 435
 Db 1578 AGCAAGCTGTGTGACGCGAACAACGCGACGCCCGGCAAAACCTTACGTGACGGCTGGCGC 1637
 Qy 436 ---LeuLysArgPheCyvArgMetAlaValGlnGlyValTrpAsnArgLysSerValPhe 454
 Db 1638 ACGGTGATGCGCGTGGAGAGAGTGTCTCACAGGAGCAACGAGAGCTTTGTGTGTTT 1697
 Qy 455 AspGlyAspArgLeuMetValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHis 474
 Db 1698 GGCAGAGGAGGTGACAGGCGTCCAAAGCTGCAAGAGAGATCTGCACTGGGCTTCTCTG 1757

Qy 475 MetAsnIleLeuLeuProAspSerHisCyvGlu-----GluTyrrTyrrThrPhePheHis 492
 Db 1758 CGG-----GCTTGGCCGAGATGTGGCCCTGAGAGCGGCGAGTCTTCAATTTTTCAC 1811
 Qy 493 LeuSerLeuGlnAspPheCyvAlaAlaLeuTyrrTyrrValLeuGlnGlyLeuGlnIleGlu 512
 Db 1812 CTTAAGCTCCAGAGCTTTCACCGCTTCTCTCTGTATACAGATGACAAATGACAGACC 1871
 Qy 513 ProAlaLeuCyvProLeuTyrrValGlnLysThrLysArgSerMetGluLeuGlnAla 532
 Db 1872 CGGAGTTGTGAGAGTTCTTTCAGATATGACAGCTCTCTGGA---GAGGCAACAAGCTCG 1928
 Qy 533 GlyPheHisIle----- 536
 Db 1929 TCTGACATTCCTTCTTCTCTCTGACGTGCTGGCGGACAGAAACCGGTTGGGCTT 1988
 Qy 537 -----HisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549
 Db 1989 GATCTTTTCAGAAACAAGATCACTTCCAGTTCAACCACTTTCGTGCGGGCTACTG 2048
 Qy 550 SerGluAspValArgArgProLeuGlnValLeuLeuGlyCyvProValProLeuGlyVal 569
 Db 2049 GCCAAAGCCGACAGAAATCTTTCGCAAGCTG-----GTGCCAAGGCTATC 2096
 Qy 570 -----LysGlnLysLeuLeuHisTrpVal-----SerLeu 579
 Db 2097 CTGAGAGAAAGGCGCAAGGCGCTG---TGGGCTCACTGTTTGTGCTAGCTGCGCTCTAC 2153
 Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGly-----Asp 591
 Db 2154 TTGAAAGCTTCACTCGGGTCCAGTCTGAGGCTTTTAAACGAGTGCATGCCATGCCACA 2213
 Qy 592 ThrLeuAspAlaPheHisCyvLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
 Db 2214 TTCTGTGATGATGCTGCGCTGATATATATGACGACAGACCAAGAGTGGGCGCTTGGC 2273
 Qy 612 LeuAsnSerPheGlnGlnValTrpLeuProIle-----AsnGlnAsnLeuAsp 627
 Db 2274 GCGAGGGGACATAGTGGAGTACCTCAAGCTGGCTTTTGCAACGCTTGTCTGCGGAC 2333
 Qy 628 LeuIleAlaSerSerPheCyvLeuGlnHisCyvProTyrrLeuArgLysIleArgValAsp 647
 Db 2334 TGCAGCGCCCTGTCTTCTGCTGCTGCATCAC-----TTCAACAGGACGTGGCCCTTGAC 2387
 Qy 648 ValLysGlyIlePheProArgAspGluSerAlaGluAlaCyvProValProLeuTrp 667
 Db 2388 CTGACACAACAACCTCAATGACTATGCGGTGAC-----GAGCTGCAGCTTGTCTT 2441
 Qy 668 MetArgAspLysThrLeuIleGlnGlnGlnTrpGluAspPheCyvSerMetLeuGlyThr 687
 Db 2442 AGCGCT----- 2447
 Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707
 Db 2448 ---CTCAGGTTATCAGACTCAGAGTCAACCAAGATCCCGACAGGGGGTGAAG 2498
 Qy 708 ThrLeuCyvAlaLysLeuArgHisProThrCyvLysValIleGlnHisLeuMet---PheArg 726
 Db 2499 GTGCTATGTAGAGAACTG---ACCAAGTAAAGTCTGACGTCTCTGGGTTTATAC 2552
 Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745
 Db 2553 AACCAACAGATATCTATATGAGAGGATATGTGCGCCAAATCTCTGATGATGACGA 2612
 Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValArgMetAla 765
 Db 2613 GCGCTTAAGCACTTAATAGGAAATAACAGATAACAATGAGTGGGGAAGTGTGTG 2672
 Qy 766 CyvGlnAlaLeuLysHisProLysCyvLeuLeuGluSerLeuArgLeuAspCyvGly 785
 Db 2673 GCTTGGCTGTGAAGAC----- 2690

Db	1197	CTGCTGGCTAACTCTCTAAGTGGAGAGGCTGCTCAAGGTCGCCGGAATTGCTACTGCT	1256
Qy	318	Arg-----AspValGlyThrGluIuIysLeuYsSerGluValValSerProArgTyr	334
Db	1257	CGCAACAGCGGTGAAGTGTCCCGCCAGGCTCGTGGCAAAAGTG	1301
Qy	335	LeuLeuValAargGlyIleSerGlyValGluInAargIleHisLeu	348
Db	1302	---CTGCTCCGGGGCTTCTCCCAAGT-----CACTGGCGGCTAATGCCGCGG	1349
Qy	349	---LeuLeuGluAargGlyIleGlyValHisGlnIuYsThrGlnIuIleuAargAlaIleMet	367
Db	1350	ATGTTCTCCCGAGCGCAGCAGCGCAGAGCATCTG-----CTCAGCAGCTGGAT	1397
Qy	368	AspAsnAargGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal	387
Db	1398	GCCAAACCCCAACCTGTGAGAGCTGTGGGGGGTGGCGCTTGTGTGATCATCTTCCGT	1457
Qy	388	AlaLeuGln---LeuGlnAspValValGlyIuSerValAlaProPheAsnGlnThrLeu	406
Db	1458	TGTTTCCAGCACTTCCAGACGGTCTTCGAGGGGCTCTCTCAGAGTTGCCGAGCTGTCT	1517
Qy	407	ThrGlyLeuHisAlaAlaPheVal-----PheHisGlnLeuThrPro	420
Db	1518	GTACCCCTGACCCGATGTCTTCTCTGCTGCTCACTAGGTGCATCTGAACGCCCGCAGCC	1577
Qy	421	ArgGlyValValAargArgCysLeuAsnLeuGluIuAargValVal-----	435
Db	1578	AGCAGCGTGGTGGAGCGCAACCGCGCAGCGCGGAAACCTTACGTGACGGCTGGCG	1637
Qy	436	---LeuIuYsArgPheCysArgMetAlaValGluGlyValTyrAsnAargYsSerValPhe	454
Db	1638	ACGCTGCATGCGCTGGAGAGGTGGCTCACCGAGGCAACGACAGAGCTCTTGTGTCTT	1697
Qy	455	AspGlyAspAspLeuMetValGlnGlyLeuGlyIuSerGluLeuAargAlaLeuPheHis	474
Db	1698	GAGCAAGAGAGTGTGACAGCGCTCGAAGCTGGAGAGAGATCTGCACGTGGGCTCTGTG	1757
Qy	475	MetAsnIleLeuLeuProAspSerHisCysGlu-----GluTyrTyrThrPhePheHis	492
Db	1758	CGG-----GCTTGGCCCGATGTGGGGCTGTAGCAGGGCAGGTCTTCAGATTTTCCAC	1811
Qy	493	LeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGlu	512
Db	1812	CTTACGCTTCAGGCGCTTCTTCAACCGCTCTTCTGCTGATGAGATGACAAAGTAGCACC	1871
Qy	513	ProAlaLeuCysProLeuTyrValGluIuYsThrIuYsArgSerMetGluLeuYsGlnAla	532
Db	1872	CGGAGTGTGTGAGGTCTTCTTGAGAAATGACGTCTCTGGA--GAGGCAACAGCTCG	1928
Qy	533	GlyPheHisIle-----	536
Db	1929	TCTGTGCATTCTCTCTTCTCTCTCTCCAGAGGCTGGGGCGGCAAGCGGTTGGGCGCT	1988
Qy	537	-----HisSerLeuTyrMetIuYsArgPheLeuPheGlyIleuVal	549
Db	1989	GATCCTTTCAAGAAACAAGATCACTTCCAGTTTCAACAACCTCTTGTTGGTGGGCTACTG	2048
Qy	550	SerGluAspValAargArgProLeuGluIuLeuLeuGlyCysProValProLeuGlyVal	569
Db	2049	GCCAAAGCCCAACAGAACTCTCTTGGCAGCTG-----GTGCCAAGCTATTC	2096
Qy	570	---LysGlnIuYsLeuLeuHisIleTyrVal-----SerLeu	579
Db	2097	CTGAGAGAGAAAGCGAAGGCGCTG---TGGGCTACCTGTGTCTAGCTGGCTCTTCA	2153
Qy	580	LeuGlyGlnIuProAsnAlaIleThrThrProGly-----Asp	591
Db	2154	TTGAAGAGCTTAACTCGGATCCAGTCTGAGAGGCTTTAACAGGTGATGCGATGCCACA	2213
Qy	592	ThrLeuAspAlaPheHisCysLeuPheGluIuThrGlnAspIuYsGluPheValAargLeuAla	611
Db	2214	TTCCTGTGATGTGCTGCGTGCATCTATGTAGACGACAGACAGAGTGGGGCGCTCGCC	2273

QY	612	LeuhsnsrPhegIngluValTrpleuProile-----AsnGlnAsnleuAsp	627
Db	2274	GCCAGGGGCATACAGTGGCGSACSTACTCCAGCTGGCTTTGCAACGGCTTGCTGCGGAC	2333
QY	628	LeuIleuAsnsrPheCyseuGlnHisCyssProTryleuAArgylsIleArgValAsp	647
Db	2334	TGCAGCGCCCTGCTCTCTCTGCTCTCAATAC-----TTCCAGACGACAGCTGGCCCTAGAC	2387
QY	648	VallysgIyIlePheProArgAspGlnserAgluValaCyssProValaProleuTrp	667
Db	2388	CTGCAGACACACAAACCTCAATGACTATAGCGGTGAG-----GAGCTGACGCTTGCTT	2441
QY	668	MetArgAspIystrIleuIleGlnGlnGlnTrpGlnAspPheCysserMetleuGlyThr	687
Db	2442	AGCGGT-----	2447
QY	688	HisProHisleuAglInleuAspLeuGlySerseerIleleuTrpGlnAArgAlaMetIys	707
Db	2448	-----CTCAGCGTTATCAGACTACAGCGCTCAACAGATCACCGAGCGGGGTGAG	2498
QY	708	ThrlleuCyssAlaIyIleuAArgHisIProThrCyssIyIleGlnTrpIleuMet---PheArg	726
Db	2499	GTGCTATGTAGAGAACTG-----ACCAAGTAAAGATCGAGAGCTTCTGGTTTATC	2552
QY	727	AsnAglInIleThrPro---GlyValGlnHisleuTrpArgIleValaMetAlaAsnArg	745
Db	2553	AACAAACCGAATACTGATATCGAGCAGCAAGTATGCGCCCAATCTGATGATGACGA	2612
QY	746	AsnleuAArgserleuAsnleuGlyGlyThrHisleuIysgIuGlnAspValaArgMetAla	765
Db	2613	GCGCTCAAGCACTTAACTTAGGGAAAAACAAATTAACAACTGAGGCGGAGACTGTGTG	2672
QY	766	CysGlnAlaIeulysHisIProIyCyseuIeulysIserleuAArgleuAspCyssGly	785
Db	2673	GCTTGGCTGTGAAGAAC-----	2690
QY	786	LeuThrHisAlaCystryleuIyIleserGlnIleleuThrThrserProIeuleuIys	805
Db	2691	-----AGACCTTCATCGTT	2705
QY	806	SerleuSerleuAlaGlyAsnIyValaThrAspGlnGlyValMetProIeuleuSerAspAla	825
Db	2706	GATGTGGAGATGGGGTATCAATGATGAAACAAAGGCGCAAGGCGCTTCGACAGAGCA	2765
QY	826	LeuArgValserGlnCyssAlaIeulysleuIyIleuGlnAspCyssGlyIleThrAla	845
Db	2766	TTGAGG---GACCAACCCAGCTTACCACTCTCAGTCTTGATTCATTAAGGATCTTCCG	2822
QY	846	ThrGlyCyssInserleuAlaSerAlaIeulysIserAsnArgserleuThrHisleuCyss	865
Db	2823	GAGGGAGGGAAGAGCGCTTGGCGGAGCGCTGTAAGCAAAACACACATGACAGTAATCTGG	2882
QY	866	LeuSerAsnAsnserleuGlyAsnGlnGlyValaAsnleuIeulysValArgserMetAspIeu	885
Db	2883	CTGACCAAAATGAATTAATGAGATCTGACAGTGTCTTCGCTGATGATCTAAGTGTG	2942
QY	886	ProHisCysserleuGlnArgleuMetleuAsnGlnCyssHisleuAspThrAlaGlyCyss	905
Db	2943	---AACCAAGAGCGCTACGGCATTTTGGCTGTATCCAAATGCGATCACAGCCAGGGAGCA	2999
QY	906	GlyPheleuAlaIeulAlaIeulMetGlyAsnserTrpleuThrHisleuSerleuSerMet	925
Db	3000	GCGAGCGCGGAGAGGCACTGCACAAAGAACACACACCACTACAGAGATTTGCTCAATGGA	3059
QY	926	AsnProValGlu-----AspAsnGlyValIyIleuIeulysCyssGln	938
Db	3060	AACCTTGATTAAGCCCGAGAGGCGCAAAGTCTTCGAGATGAGGAAGAAATCATGTGCTT	3118
QY	939	ValMetArgIeuProserCyssHisleuGlnAspIeu-----GlyIeuValIyCyssHis	956
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Qy 957 LeuThrAlaAlaCyS-----CyGluSerLeuSerCyVal 968
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RESULT 15
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; Sequence 42, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
; US-09-340-620A-42

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Score: 379.50 Matches: 253
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Best Local Similarity: 23.23% Mismatches: 416
Query Match: 5.36% Indels: 273
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US-10-066-521-6 (1-1344) x US-09-340-620A-42 (1-4141)
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Qy 26 PheGlnThrPheIyGluLeuLeuIySylSylSerSerGluSerThrCySeriIle 45
Db 487 -----AGAGCAAAAGCGAGAGGTGTCTGATCTCTCTTACGTGACGTGACG- 533
Qy 46 ProGlnPheGluIleGluAsnAlaAsnValGluCySLeuAlaLeuLeuIleuHisGluTyr 65
Db 534 -----CAGCTGAGAGATGCTTACGTGAC--CTCAGAGCTG----- 566
Qy 66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85
Db 567 -----TGCCTCTCAGAAATTTGGCTTCTCCCTTCCACACTATTGCG 608
Qy 86 ThrLeuSerGluIyValArgAspPheMetLeuIySylSylSerGlnAlaMetGluGlnIu 105
Db 609 ACCAAACTATCTGCTCAATATCTGACCCAGTATACCAACAGCTGACGACCA 668
Qy 106 GlyAlaThrAlaAlaGluThrGluGluGlnIuIleSerGlnAlaMetGluGlnIu 125
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Qy 126 AlaThrAlaAlaGluThrGluGluGlnIuIleGlyIyAspThrTrpAspTyrIySer 145

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Db 684 AAGTTCACTGTGTGTGACGACCAAGAGAGACTG-----CTGCTGAGGAGAGC--- 734
Qy 166 AlaSerTrpProGluMetGlnThrLeuAlaGly-----AlaPheAspSerAspArgTrp 183
Db 735 -----TATATGACACACTATGAGGGGCTGTAGGCTTCAACATGAAAACCG 782
Qy 184 GlyPhe-----Arg 186
Db 783 GGCAGCCCTAGAGAGCTGATTCCTCTGACCAACAGTACGAGGCTCTTCAACAGCAT 842
Qy 187 ProArgThrValValLeuHisGlyIySylSerGlyIleGlyIySylSerAlaLeuAlaArg 206
Db 843 GCGGAGCTGTCTTCTGTTGGGAGACCGGAGAGGGGAGGATTCATGCTGTGACAGG 902
Qy 207 IleValIleuCySTrpAlaGlnGlyIyLeuTyrglnIyMetPheSerTyrgValPhePhe 226
Db 903 TTGCAGAGCCCTGTGGGCTCAGGAGGTG---ACCTCAGACGCCAATTTCTTCCAC 959
Qy 227 LeuProValArgGluMetGlnArgIySylSylSer-----SerValThrGluPhe 243
Db 960 TTCGCTGCTCCGATGTTCACTGCTTCAAGAGAGGACATGCTGATCTCAGAGACCTG 1019
Qy 244 IleSerArgIuTrp-----ProAspSerGlnAlaProValThrGluIleMet 259
Db 1020 CTCTTCAAGCATTTCTGTCTACCCGAGAGAGACCCGAGAGGTCTTCTCTTCTGCTG 1079
Qy 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer----- 277
Db 1080 CGCTTCCACACAGCGCTTTCATCTTTACCGCTCGATGAGTACTGCTACAGACTTC 1139
Qy 278 ValLeuAsnAspThrIySylLeuCySylAspTrpAlaGluIyGlnPheProPheThr 297
Db 1140 GACCTGAGCCGCGGCGCATAGCTGTGCTGCCCTG---GAGCGGCTCACCTGTGCTC 1196
Qy 298 LeuIleArgSerLeuLeuArgIyValLeuLeuProGluSerPheLeuIleValThrVal 317
Db 1197 CTGCTGCTTAACTCTTAAAGTGGAGAGCTGTCAAGGTTGCGGCAATTTCTCACTCT 1256
Qy 318 Arg-----AspValGlyThrGluIySylSylSerGluValIleSerProArgTyr 334
Db 1257 CGCACAGCGCTGAGAGTCCCGCGCAGCTCTGCGCAAAAGGTG----- 1301
Qy 335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeu----- 348
Db 1302 ---CTGCTCGGGGCTTCTCCCAAGT-----CACTGCGGCGCTATGCCCGCGG 1349
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Db 1350 ATGTTCCCGCGAGCGCACAGCGCAGAGCATGTG-----CTGCACAGCTGAT 1397
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Qy 388 AlaLeuGln---LeuGlnAspValValGlyIySylSerValAlaProPheAsnGlnThrLeu 406
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Qy 407 ThrGlyLeuHisAlaAlaPheVal-----PheHisGlnLeuThrPro 420
Db 1518 GTGACCTCGACCGATGTTCTTCTGTCTGTCTGATCACTGAGTGCATTCGACGCCGACGCC 1577
Qy 421 ArgGlyValValArgArgCySLeuAsnLeuGluIuArgValVal----- 435
Db 1578 AGCAGCCTGTGTGCGGACAGCGGACCGGACCGGCGGAAACCTTACGTGACGCTGGCGC 1637
Qy 436 ---LeuIySylArgPheCySylMetAlaValGluIyValTrpAsnArgIySerValPhe 454
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Qy 455 AspGlyAspArgLeuMetValGlnGlyLeuGlyGlnSerGluLeuValGlnLeuPheHis 474
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Qy 475 MetAsnIleLeuLeuProAspSerHisCysGlu-----GluTyrTyrThrPhePheHis 492
Db 1758 CGG-----GCTTGGCCGATGATGGGCCCTGAGCAGGCGCGAGCTTACGAAATTTTTCAC 1811
Qy 493 LeuSerLeuGlnAspPheCysValAlaLeuTyrTyrValLeuGlnGlyLeuGlnIleGlu 512
Db 1812 CTTACGCTCCAGCGCTTCTTACCGCTTCTTCCGTGAGCAATGACAAAGTAGACACC 1871
Qy 513 ProAlaLeuCysProLeuTyrValGlnGlyLeuThrLeuValSerMetGlnLeuGlnAla 532
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Qy 533 GlyPheHisIle----- 536
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Db 1989 GATCCTTTCAGGAACAAGATCACTTCCAGTTTCACCAACTCTTCTGTGGCGGCTACTG 2048
Qy 550 SerGluAspValArgArgProLeuGlnValLeuLeuGlyCysProValProLeuGlyVal 569
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Qy 570 -----LysGlnValLeuLeuHisThrVal-----SerLeu 579
Db 2097 CTGAGAGAGAGCGGAGGCGCTG---TGGGCTCACTGTTCGTAAGCTGCGCTCTTAC 2153
Qy 580 LeuGlnGlnGlnProAsnAlaThrThrProGly-----Asp 591
Db 2154 TTGAAGAGCCCACTCGGCTCCAGTCTGAGGCTTTAACAAGTCGATGCCATGCCACA 2213
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspLysGlnPheValArgValAla 611
Db 2214 TTCCTGTGATGCTGCGCTGATCATGAGACGACGACGAGAGTGGCGGCTCGCC 2273
Qy 612 LeuAsnSerPheGlnGlnValThrLeuProIle-----AsnGlnAsnLeuAsp 627
Db 2274 GCCAGGCGCATCACTGCGGATCACTCACTGAGCTTTTGCAACGCTTGTCTGCGGAC 2333
Qy 628 LeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAsp 647
Db 2334 TGCAGCGCCCTGTCTCTGCTGCTGATCAC-----TTCACAGGCACTGCGCTTAC 2387
Qy 648 ValLysGlyIlePheProArgAspGlnSerAlaGlnAlaCysProValProLeuTyr 667
Db 2388 CTGACACAACAACAACCTCAATGATCATGCGTGGAG-----GAGCTGCAAGCTTGTCTT 2441
Qy 668 MetArgAspLysThrLeuIleGlnGlnIleThrGlnAspPheCysSerMetLeuGlyThr 687
Db 2442 AGCCGT----- 2447
Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLys 707
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Qy 708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet---PheArg 726
Db 2499 GTGCTATGTGAGAACTG-----ACCAAGTAAAGATCGAAGCTTCTGGGTTTATAC 2552
Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuThrArgIleValMetAlaAsnArg 745
Db 2553 AACCAACGATTAATGATATGATGAGCCAGTATGTGGCCCAAAATCTGGATGAATGCAGA 2612
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGlnAspValArgMetAla 765
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Qy 766 CysGlnAlaLeuLysHisProLysCysLeuLeuGlnSerLeuAlaGlyLeuAspCysGly 785
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Db 2691 -----AGCACTCCATGCTT 2705
Qy 806 SerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAla 825
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Qy 826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAla 845
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Qy 957 LeuThrAlaAlaCys-----CysGlnSerLeuSerCysVal 968
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Search completed: February 4, 2005, 18:11:52
 Job time : 670 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: February 4, 2005, 17:27:06 ; Search time 1551 Seconds

(without alignments)
4987.568 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 7074
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSMSCAGLGLGVLS 1344

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 4313806 seqs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=std.rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HARPSIZE=500 -MINLEN=0
-MALIGN=200000000 -USER=US10066521@cgn2_1.1.876 @runac_04022005_114554_4440
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Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	7074	100.0	4035	14	US-10-124-498-5
2	7074	100.0	4035	14	US-10-066-521-5
3	5756	81.4	3489	17	US-10-416-642-3
4	5756	81.4	3926	15	US-10-216-645-1
5	5741.5	81.2	3885	18	US-10-860-761-3
6	5741.5	81.2	3900	17	US-10-399-443-23
7	5741.5	81.2	3900	17	US-10-677-943-23
8	5683.5	80.3	3830	15	US-10-216-645-3
9	5120	72.4	3226	17	US-10-092-900A-347
10	2688	38.0	3447	17	US-10-399-443-5
11	2688	38.0	3447	17	US-10-677-943-5
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14	1885.5	26.7	3521	18	US-10-794-342-2
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18	1434	20.3	2982	14	US-10-066-521-25
19	1434	20.3	2985	10	US-09-965-621-15
20	1434	20.3	2985	17	US-10-407-866-15
21	1434	20.3	2985	18	US-10-781-294-15
22	1402	19.8	2775	17	US-10-357-820-51
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31	1314.5	18.6	2883	17	US-10-161-693-3
32	1313.5	18.6	3540	18	US-10-794-342-7
33	1304.5	18.4	3218	17	US-10-407-866-67
34	1303.5	18.4	3186	14	US-10-124-498-17
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39	1255	17.7	3102	13	US-10-027-629-6
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42	1255	17.7	3857	13	US-10-027-629-4
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45	1242	17.6	3466	17	US-10-108-260A-718

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-367001
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US/10/124,498
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25

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; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4032)
US-10-124-498-5

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

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QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db 121 ACCCAAGCTCTTATTCCACAGTTTGAAATTCAGAAATGCCAAGTGGAAATGCTGGCACTC 180

QY 61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
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QY 121 MetGluGluGluGlyAlaThrAlaAlaGluThrGluGluGluGluIleSerGlyAspThr 140
Db 361 ATGGAACAAGAAAGGCGCACAGCAGCAGACAGAAACAGAACTGAGGAGACACA 420

QY 141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
Db 421 TGGGACTTACAGAGATGACGTGATGACCAAAATTCGCTGAGAGAGATGATGCTGTAGT 480

QY 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
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QY 181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
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QY 201 SerAlaLeuAlaArgAlaGluValLeuLysSerTrpAlaGluGluGlyLysLeuTyrGlnGlyMet 220
Db 601 TCGGCTCTAGACCAAGAGATGCTGCTGCTGGCGCAGAGGTGACTCTTACCAAGGAATG 660

QY 221 PheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSerVal 240
Db 661 TTCTCCCTACGCTCTTCTCTCCCGTTAGAGATGACGCGAAAGAAAGAGACAGTGTCT 720

QY 241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
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QY 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
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QY 321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyIle 340
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QY 341 SerGlyGluGluArgIleHisLeuLeuLeuGluLysGlyIleGlyGluHisGlnLysThr 360
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QY 381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
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QY 401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
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QY 441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
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QY 461 ValGlnGlyLeuGlyGlySerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
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RESULT 2
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; Sequence 5, Application US/1006521
; Publication No. US2003002757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 0734-34001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-066-521-5

Alignment Scores:

Pred. No.:	0	Length:	4035
Score:	7074.00	Matches:	1344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

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Db 3061 GCACTCTCTTGCCCTTCTCGCAACCGGATCTGACAGACTTAACCTGGGTGAGAAAT 3120
Qy 1041 AsnPheSerProLybGlyMetMetLybLeuCysSerAlaPheAlaCysProThrSerAsn 1060
Db 3121 AACTCAGTCCCAAGAGATATGAAGCTGTGTGTGCTTGGCTTGTCCACGCTTAAC 3180
Qy 1061 LeuGlnIleIleGlyLeuTrrLybTrrGlnTrrProValGlnIleArgLybLeuLeuGlu 1080
Db 3181 TTACAGATTAATGGGCTGTGAAATGGCAATGCTGTGCAATTAAGAACTGCTGAG 3240
Qy 1081 GluValGlnLeuLeuLybProArgValValIleAspGlySerTrrHisSerPheAspGlu 1100
Db 3241 GAAGTGAGCTTAACCAAGCCCGAGTGTAAATTAAGTGAAGTGAATCTTTGATGA 3300
Qy 1101 AspAspArgHisLybIleGlyLeuThrPheArgLeuProGluSerArgAlaTrrProCys 1120
Db 3301 GATGACCAACCAAAATGGAATTACTTTCGGGCTCCCTGAAGCCGGGCAATGGCAATG 3360
Qy 1121 AlaLeuLeuTrrGlyMetAsnProGluGlnLybLybAspValSerLeuLeuAlaGlyAsp 1140
Db 3361 GCTTGTGTGGGATTAACCAAGAGCAAGAAAGCGTGTGTCTTGTGCTGAGAAC 3420
Qy 1141 PheLybSerSerTrrArgPheAlaLybSerLeuCysLeuAlaTrrAlaAsnGlyGluSer 1160
Db 3421 TTCAAGAGCATTAACCAATTTGCCAAGTCTGTGCTGGCCAGCGCAAAATGTGATGCC 3480
Qy 1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGlnHisLyb 1180
Db 3481 CAGAGAGTTGAACAAGTGACAGAGCTCCCGCAACCAATGAGGAGGAGCAACAGCAAA 3540
Qy 1181 GlnAspLybMetLeuSerValGlyTrrSerGlyAlaTrrPserGluThrAlaGluLeuGlu 1200
Db 3541 CAAGTAATAATGTTGAAGTGTGAATATCCGAGAGCTGTGTGAACTGTGAGGCTCAAA 3600
Qy 1201 GlyLeuGlySerAsnSerAlaAspHisAspHisAspGlyMetAlaTrrPserLeuGlyArg 1220
Db 3601 GGGCTGTGATCAACAGTGTGATCAATGACACGAGGATTAAGGCTGTGACTAGAGAGA 3660
Qy 1221 GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrAlaValCysProGly 1240
Db 3661 GAGCTGAGCTGAGAGGGCTGTGTGTCAACAGTGTGATGACACAGCGGTGTGTCTGTGT 3720
Qy 1241 HisTrrGluArgGluGlySerArgGlyTrrProCysLeuAsnSerAlaAspAspHisSerGly 1260
Db 3721 CACTGGAGCGGCTGGGCTTGAAGGCTGGGTGTCTTAACAATGCTGAAGACAGCGGT 3780
Qy 1261 ValSerTrrPserLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280

Db 3781 GTGCTCGGTACTGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCACAGTCGTGATGAC 3840
Qy 1281 HisSerGlyValAlaTrpSerLeuGlyValAlaGlyLeuGluGlyLeuValSerAsnSer 1300
Db 3841 CACAGCGGTGTGGCTGTGTCTGCTGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCACAGCT 3900
Qy 1301 AlaAspAspHisSerGlyValSerTrpSerLeuGlyValAlaGlyLeuGluGlyLeuVal 1320
Db 3901 GCTATGACCAACACGCGGTGTGTCTGTGTCTGCTGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy 1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyValAlaGlyLeuGlu 1340
Db 3961 TCCACAGCTGTGTATGACCAACGCGGTGTGTCTGTGTCTGCTGGAGCGGCTGGGCTCGAG 4020
Qy 1341 GlyLeuValSer 1344
Db 4021 GGGCTGGGTGTCT 4032
RESULT 3
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: RANKUMAR, Jayalaxmi
; APPLICANT: ARVIZU, Chandra
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0842 PCT
; CURRENT APPLICATION NUMBER: US/10/416,642
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: 60/249,407
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3
Alignment Scores:
Pred. No.: 0 Length: 3489
Score: 5756.00 Matches: 1102
Percent Similarity: 95.34% Conservative: 2
Best Local Similarity: 95.16% Mismatches: 0
Query Match: 81.37% Indels: 54
DB: 17 Gaps: 1
US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)
Qy 1 MetGluGlyAspLysSerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGlu 20
Db 1 ATGGAAGAGCAAAATGCTCACCCTTTTCCAGTCAAGGCTGCAATGGTGTCTCTATGAG 60
Qy 21 LeuAspLysGluGluLupheGlnThrPheLysGluLeuLeuLysLysSerSerGluSer 40
Db 61 CTAGACAGAGAAATTTCAACATTCAGAGAAATTAATAAGAAATCTTCAGAAATCG 120
Qy 41 ThrThrCysSerTrpProGlnPheGluLuiLegLubAsnAlaAsnValGluCysLeuAlaLeu 60
Db 121 ACCACAGCTCTATTTCACAGATTGAAATCGAAGATCGCAACGTGGAATGTCTGGCATC 180
Qy 61 LeuLeuHisGluTrpTrpGlyValAserLeuAlaTrpAlaThrSerTrpSerTrpPheGlu 80
Db 181 CTCTTGATGATGATTTATGAGACATCGCTGGCTGAGCTACGTCCATTAAGCATCTTGA 240
Qy 81 AsnMetAsnLeuArgTrpThrLeuSerGluLysValAlaArgAspMetLys----- 96
Db 241 AACATGAACCTGCGAACCTCTCGAGAGAGCGAGGATGACATGAAGAAATTCACCGAA 300

Qy 96 ----- 96
Db 301 GATCTGAAGCAACGATGACTGACCAAGACCAAGCAAGAAAAATGCCAGAAAAATAA 360
Qy 96 ----- 96
Db 361 TATGCACTAGACTTAAGCTTATCTTGGGGGTCTGCACTCTCTGACTGGAATTAATAAC 420
Qy 97 -----LysIleSerGlnAlaMetGluGluGly 106
Db 421 AAGTATGTGGAAATTCATTCTTCTTTGAGAAATTTCAAGCTATGGAACAGAAAGT 480
Qy 107 AlaThrAlaAlaGluTrpGluGluGlnGluLuiLerSerGlnAlaMetGluGluGlyAla 126
Db 481 GCCACAGACAGACAGACAGAAACAAAGAAATTTCAAGCTATGGAACAGAAAGTGGCC 540
Qy 127 ThrAlaAlaGluTrpGluGluGlnGlyHisGlyValAspTrpTrpAspTrpLysSerHis 146
Db 541 ACAGACAGACAGACAGAAACAAAGAACTGAGGTACATGGACTACAGAGTTC 600
Qy 147 ValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAla 166
Db 601 GTATGACCAAAATTCGTGAGAGAGAGAGATGATGCTGATGTTTGAAGACATGCTGCT 660
Qy 167 AspTrpProGluMetGlnThrLeuAlaGlyValaPheAspSerAspArgTrpGlyPheArg 186
Db 661 GACTGGCCGGAAGCAAGCGTGGCTGTGCTTTGATTTCAGACCGGTGGGCTTCCGG 720
Qy 187 ProArgThrValAlaLeuHisGlyLysSerGlyLuiLysSerAlaLeuAlaArgArg 206
Db 721 CTTGCAAGGTGTTCTGCAAGGAAATCGAGAAATGGAATGGCTCTAGCCAGAAAG 780
Qy 207 IleValLeuCysTrpAlaGlnGlyGlyLeuTrpGlnGlyMetPheSerTrpValaPhePhe 226
Db 781 ATCGTGCTGTGTGGGGCAAGGTGACTGTACAGAGGAATGTTCTCTAGCTTCTTC 840
Qy 227 LeuProValArgLuiMetGlnArgLysLysGluSerValThrGluPheLysSerArg 246
Db 841 CTCCCGCTTGAAGATGACGCGGAAAGAGAGCATGTCACAGAGTTTCATCTCCAGG 900
Qy 247 GluTrpProAspSerGlnAlaProValThrGluLuiLerSerArgProGluArgLeuLeu 266
Db 901 GAGTGGCAAGCTCCAGGCTCCGGTACGAGATCATGTCCGACCAAGAAAGCTGTGG 960
Qy 267 PheIleLeuAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspTrpLysLysCys 286
Db 961 TTTCACTATTGACGTTTCAATGACTGTGGCTCTCTCTCAAAATGACAAAGCTTGC 1020
Qy 287 LysAspTrpAlaGluLysGlnProPheThrLeuLuiLerSerLeuLeuArgLysVal 306
Db 1021 AAAGACTGGCTGAGAGCAGCCTCCGTTCACTCATACGAGTGTGTGAGAGAGTGC 1080
Qy 307 LeuLeuProGluSerPheLeuLuiLerValThrValArgAspValGlyThrGluLysLeuLys 326
Db 1081 CTGCTCCCTGAGTCTTCTGATGTCACCGTCAAGACGTGGGCAAGAGACTCAAG 1140
Qy 327 SerGluValAlaSerProArgTrpLeuLeuValArgGlyLuiLerSerGlyGluGlnArgLys 346
Db 1141 TCAGAGGTGTGTCTCCCGTTACTCTTGTAGAGAAATCTCCGGGAAACAAAGATC 1200
Qy 347 HisLeuLeuLeuGluArgGlyLuiLerGluHisGlnLysThrGlnGlyLeuArgAlaLys 366
Db 1201 CACTTGCTCTTGAGCCGGGATTTGGAGCATCAGAAAGACAAAGAGTGGCGCATC 1260
Qy 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValaProAlaValaGlySerLeuLuiLerCys 386
Db 1261 ATGAACAACCGTGAAGCTGCAACAGTGCAGAGTGCACCGCGGTGGCTCTCATCTGC 1320
Qy 387 ValAlaLeuGluLeuGlnAspValAlaGlyLuiSerValAlaProPheAsnGlnThrLeu 406
Db 1321 GTGGCTCTGACGTGCAAGAGCTGTGGGAGAGAGCTCCGCCCTTCAACCAACGCTC 1380
Qy 407 ThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValaLysArg 426

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Db      1381  ACAGGCGCGACGCGCTTTGTGTTTCATGAGCTCACCCCTCGAGGGGTGCTCGGCGC 1440
Qy      427   CysleuenuleuugluuargvalValleuysarPheCy8arGmeAlaValGluGly 446
Db      1441  TGTCTCAATCTGGAGAAAGAGTGTCTTGAGGCGCTTCCGTAATGCTGTGGAGGGA 1500
Qy      447   ValTrrAsnArgLysSerValPheAspGlyAsPheLeuMetValGluGlyGlu 466
Db      1501  GTTGGAATAGGAATCACTGTTTCAACGTTGACACCTCATGTTCAAGAGCTCGGGAG 1560
Qy      467   SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
Db      1561  TCTAGGCTCCGTCCTGTTTCAATGAAACATCTTCTCCAGACAGCCATGTAAGAG 1620
Qy      487   TyrTyrThrPhePheHisLeuSerLeuGlnAsPheCysAlaAlaLeuTyrTyrValLeu 506
Db      1621  TACTAACACCTTCTTCCACTGATCTCCAGAGCTTCTGTGCGCTTGTACTACGTGTTA 1680
Qy      507   GluGlyLeuGluGluIleGluProAlaLeuCysProLeuTyrValGluYsrThrLysArgSer 526
Db      1681  GAGGCGCTGGAAATCGAACCGCTCTCTGCGCTGTGACGTTGAGAGACAAAGAGTCC 1740
Qy      527   MetGluLeuLysGluAlaGlyPheHisIleHisSerLeuTyrMetLysArgPheLeuPhe 546
Db      1741  ATGAGAGCTTAACAGGAGGCGCTTCCATATCCACTGCTTGGATGAAGCGTTTCTGT 1800
Qy      547   GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566
Db      1801  GGCTCTCGTGAACGAGAGCGTAAGAGGCGCACGTGAGGTCTGCTGGGCTGTCCGCTCC 1860
Qy      567   LeuGlyValLysGluIleLysLeuHisIleTrrValSerLeuLeuGluGluGlnIleProAsnAla 586
Db      1861  CTGGGGGGTGAAGCAGAGACTCTGACATGGGCTCTCTGTGGGGTCAAGCATATATCC 1920
Qy      587   ThrThrProGlyAsPheThrLeuAspAlaPheHisCysLeuPheGluThrGlnAsPheGlu 606
Db      1921  ACCAGCCCGAGAGACACCTCGAGCGCTTCCACTGTCTTTCGAGACCTCAAGACAAAG 1980
Qy      607   PheValArgLeuAlaLeuAsnSerPheGluGluValTrrLeuProIleAsnGlnAsnLeu 626
Db      1981  TTTGTTCGCTTGGCATTTAAACAGCTTCCAAAGAGTGTGCTTCCATTTAAACAGAACCTG 2040
Qy      627   AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db      2041  GACTGTAGAGCATCTCTCTGCTCCAGACATGTCGTAATTTGCGGAAATTCGGGTTG 2100
Qy      647   AspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValProLeu 666
Db      2101  GATGTCAAAGGAGCTTCCCAAGAGATGATCCGCTGAGCATGTCTGTGCTCCCTCTA 2160
Qy      667   TrpMetArgAspLysThrLeuIleGluGluGlnTrrGluAsPheCysSerMetLeuGly 686
Db      2161  TGGATGGCGGATTAAGACCTCATTTGAGGAGCATGGGAAAGATTCTGTCCATGCTTGGC 2220
Qy      687   ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db      2221  ACCACCCACACCTGGCGGACATGACCTGGGAGAGCATCTGACAGACGGGCGCCATG 2280
Qy      707   LysThrLeuCysAlaLysLeuArgHisIleProThrCysLysIleGlnThrLeuMetPheArg 726
Db      2281  AAGACCTGTGTGTCCAGCTAGGCAATCCACCTGCAAGATACAGACCTCATATGTTTGA 2340
Qy      727   AsnAlaGlnIleTrrProGlyValGlnHisLeuTrrArgIleValMetAlaAsnArgAsn 746
Db      2341  AATGCAACGATTAACCTCGTGTGTGACAGCACTTGAAGAAATGTCATAGCCCAACGTAAC 2400
Qy      747   LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCys 766
Db      2401  CTAAGATCCCTCAACTTGGAGGACCCACCTGAAGAAAGAGATGAAGATGGCGGT 2460
Qy      767   GluAlaLeuLysHisIleProLysCysLeuLeuGluSerLeuArgLeuAspCysGlyLeu 786

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Db      2461  GAAGCTTTAAACACCCAAATGTTTGTGAGATCTTTAGAGGCTGGAATGCTGTGATG 2520
Qy      787   ThrHisAlaCysTyrTrpLeuValIleSerGlnIleLeuThrTrpSerProSerLeuYsSer 806
Db      2521  ACCAGTCCCTGTATCTTAAGATCTCCAAATCTCTTACGACTCTCCCAAGCTGAAATCT 2580
Qy      807   LeuSerLeuAlaGlyAsnLysValThrAspGluGlyValMetProLeuSerAspAlaLeu 826
Db      2581  CTGAGCTGGCAGGAAACAGAGTGAACAGACGAGGAGTAATGCTCTCAGTGAATGCTTGG 2640
Qy      827   ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
Db      2641  AAGATCTCCAGTGGCGCTTGCAGAGCTGAATCTGAGAGCTGTGGCATCAACACAG 2700
Qy      847   GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db      2701  GATTGCCAGATCTGGCTTACGCTTCCGCTTCAAGCAACCGAGCTTGAACACTGTGGCTTA 2760
Qy      867   SerAsnAsnSerLeuGluAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
Db      2761  TCCAAACACAGCTGGGGAAGAGTGTATATCTACTGTGTCAATCAATGAGGCTTCC 2820
Qy      887   HisCysSerLeuGluArgLeuMetLeuAsnGlnCysHisIleuAspThrAlaGlyCysGly 906
Db      2821  CACTGTAGTCTGACAGAGCTGATGCTGAATCAGTGCACCTGGACACCGCTGGCTGTGCT 2880
Qy      907   PheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisIleuSerLeuSerMetAsn 926
Db      2881  TTTCTTGACCTTGGCTTATGTTATGTTACTCAATGAGCTGAGACCTGAGCTTAAGCATGAC 2940
Qy      927   ProValGluAspAsnGlyValLysLeuLeuCysGluValMetCysArgLysProSerCysHis 946
Db      2941  CTTGTGAAGACATATGCGCTGAACCTTGTGCGAGGCTGACAGAGACATCTTGTCTAT 3000
Qy      947   LeuGlnAspLeuGluLeuValLysCysHisIleuThrAlaAlaCysCysGluSerLeuSer 966
Db      3001  CTCGAGAGCTGAGATTGTAAAGTTCATCTCACCGCGCGTGTGAGAGATGCTGTGCC 3060
Qy      967   CysValIleSerArgSerArgHisIleuLysSerLeuAspLeuThrAspAsnAlaLeuGly 986
Db      3061  TGTGTGATCTGAGAGAGACACCTGAAGAGCTTGAATCTCAGACAGACATGCTTGAGT 3120
Qy      987   AspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArg 1006
Db      3121  GACGCTGGGTTGCTGTCACTGTGCGAGGACTGAAGACAAAGACAGTCTTCAACAGA 3180
Qy      1007   LeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
Db      3181  CTCGGGTTGAAGGATGAGACTGATCTTGAATGCTGTGAGGACATCTCTGCGCCCTT 3240
Qy      1027   SerCysAsnArgHisIleuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db      3241  TCTGCAACCGGCATCTGACCAAGTCTAAACCTGTGTGCAAGTAATCTTCAAGTCCAAAGA 3300
Qy      1047   MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
Db      3301  ATGATGAAGCTGTGTGGCTTGTGCTTGTCCAGCTTCACTTAACAGATTAATGGGCTG 3360
Qy      1067   TrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLys 1086
Db      3361  TGGAAATGGCAGTACCTGTGCAATTAAGAAAGTGTGGAGGAAAGTGCACCTACTCAAG 3420
Qy      1087   ProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db      3421  CCCGAGTCTGAATTAAGACGTAATGTGCATTTCTTATGAATGAACCCGGTAC 3474

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RESULT 4

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US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LBSL, MONIKA

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APPLICANT: PETERS-KOTTIG, MICHAEL
APPLICANT: BECKMANN, GEORG
TITLE OF INVENTION: HUMAN MATER PROTEINS
FILE REFERENCE: SCH-1910
CURRENT APPLICATION NUMBER: US/10/216,645
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3926
TYPE: DNA
ORGANISM: Homo sapiens
US-10-216-645-1

Alignment Scores:
Pred. No.: 0 Length: 3926
Score: 5756.00 Matches: 1102
Percent Similarity: 95.34% Conservative: 2
Best Local Similarity: 95.16% Mismatches: 0
Query Match: 81.37% Indels: 54
DB: 15 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrglyLeuGlnTrpCysLeuTyrglu 20
DB 1 ATGGAAGAAGCAATATGCTCACTTTCCAGCTACGGGCTGCAATGGTGTCTCTAGAG 60

QY 21 LeuAspLysGluLysPheGlnThrPheLysGluLeuLysLysLysSerSerGluSer 40
DB 61 CTACACAGAGAGAAATTCACACATTCAGAAATTTACTAAAGAAATTTCTCAGAAATCG 120

QY 41 ThrThrCysSerTleProGlnPheGluLysLeuAsnValGluCysLeuAlaLeu 60
DB 121 ACCCAAGCTCTATTCACAGTTTGAAATCGAAGATCGAACGAGATGCTGGCACTC 180

QY 61 LeuLeuHisGluTyrglyAlaSerLeuAlaTrpAlaThrSerTleSerTlePheGlu 80
DB 181 CTCCTGGATGAGTATTTAGAGATCGCTGGCTGGCTAGTCAATTAGCATCTTTGAA 240

QY 81 AsnMetAsnLeuAlaGlnThrLeuSerGluLysAlaArgAspMetLys----- 96
DB 241 AACATGAACCTCGCAACCTCTCGAGAGAGCAGCGATGACATGAAAAATTCACACGAA 300

QY 96 ----- 96
DB 301 GATCTGAGCAAGATGATGACCAAGACCAAGCAAGAAAGTGCAGAAATPAA 360

QY 96 ----- 96
DB 361 TATGCGATGACTAAGCTTATCTTGGGGTGTCTGACATCTCTGACTGGAATPAAACAC 420

QY 97 -----LysIleSerGlnAlaMetGluGlnGluGly 106
DB 421 AAGTATGTTGGAATTCATCTTCTTTTGCAAGAAATTCACAACTATGGAACAGAAAGGT 480

QY 107 AlaThrAlaIleGluThrGluGluGlnGluLysSerGlnAlaMetGluGlnGluGlyAla 126
DB 481 GCCACAGAGACAGACAGAAAGCAAGAAATTCACAACTATGGAACAGAAAGGTGCC 540

QY 127 ThrAlaIleGluThrGluGlnGluGlnGlyHisGlyGlyAspThrTrpAspTyrglySerHis 146
DB 541 ACAGACACAGACAGACAGAAAGCAAGACATGAGGTGACATGGGACTTCAAGAGTAC 600

QY 147 ValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAla 166
DB 601 GTGATGACCAAAATTCGCTGAGAGAGAGATGATGATGATGATTTGAAAACACTGCTGCT 660

QY 167 AspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArg 186
DB 661 GACTGCGCGGAAATGCAACGTTGCTGTGCTTTTGTATTCAGCCGGTGGGCTTCCGG 720

QY 187 ProArgThrValValLeuHisGlyLysSerGlyTleGlyLysSerAlaLeuAlaArgArg 206
DB 721 CTCGACAGCGGTGTTCGACAGGAAAGTCAAGAAATTCGAGCTTACGACAGAGAG 780

QY 207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrglnGlnLysPheSerTyrglyAlaPhePhe 226
DB 781 ATCGTGTGTGTGGGGCAAGGTGACCTTACCAAGGAAATGTTCTTCAAGTCTTCTTC 840

QY 227 LeuProValArgGluMetGlnArgLysGlyLysSerSerValThrGluPheIleSerArg 246
DB 841 CTCCTCCCTTGAAGATGACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

QY 247 GluTrpProAspSerGlnAlaProValThrGluLysSerArgProGluArgLeuLeu 266
DB 901 GAGTGGCCAGACCTCCAGGCTCCGGTGAAGAGATGATGATGATGATGATGATGATGAT 960

QY 267 PheIleIleLeuArgLysPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCys 286
DB 961 TTCATTCATTTGACGGTTTCGATGACCTGGCTGTGCTTCAACAAATGACACAAAGCTTGC 1020

QY 287 LysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgVal 306
DB 1021 AAAGACTGGGCTGAG 1080

QY 307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLys 326
DB 1081 CTGCTCCCTGAGTCTTCTGATGCTGACCGTCAAGAGAGAGAGAGAGAGAGAGAGAG 1140

QY 327 SerGluValValSerProArgTyrglyLeuValArgGlyLysSerGlyGlnArgLys 346
DB 1141 TCAGAGGTCTGTCTCCCGTACCTGTGTAGTGAAGAAATCTCCGGGAGAAAGAAATTC 1200

QY 347 HisLeuLeuLeuGluArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 366
DB 1201 CACTGCTCTTGTAGCGCGGAGATTTGTGACATCAAGAGAGAGAGAGAGAGAGAGAG 1260

QY 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386
DB 1261 ATGAAACAACCGTAGCTGCTGCACAGTGCAGAGTCCCGCGGGGCTCTCATCTGC 1320

QY 387 ValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
DB 1321 GTGGCCCTGAGCTGAG 1380

QY 407 ThrGlyLeuHisAlaIlePheValPheHisGlnLeuThrProArgGlyValAlaArgArg 426
DB 1381 ACAGGCTTGAACGCGCTTTTGTGTTCATCAAGCTCACCCCTGAGGCGGTGCGGCGC 1440

QY 427 CysLeuAsnLeuGluGluArgValAlaLeuLysArgPheCysArgMetAlaValGluGly 446
DB 1441 TGTCTCAATCTGAGAGAAAGGTGTCTGAAGGCTTTCGCGTATGGCTGTGAGAGGA 1500

QY 447 ValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlu 466
DB 1501 GTGTGAATGGAAGTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560

QY 467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
DB 1561 TCTGAGCTCGGTGCTCTGTTTCAATGAAATCTTCTCCAGAGAGAGAGAGAGAGAGAG 1620

QY 487 TyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrglyValLeu 506
DB 1621 TACTACACCTTCTTCCACTCAAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

QY 507 GluGlyLeuGlnLysGluProAlaLeuCysProLeuTyrglyGlyLysThrLysArgSer 526
DB 1681 GAGGCGCTGGAATTCAG 1740

QY 527 MetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuThrMetLysArgPheLeuPhe 546
DB 1741 ATGAGGCTTAAACAGGAGGCTTCCATATCACTGCTTGGATGAAGAGCTTCTTGTTC 1800

QY	544	GIyleuValSerGIuaAspValArgArgProIeuGIuValIleuLeuGIyCyAspProValPro	566
Db	1801	GSccCTCGAGGAAAGCTAAAGAGGCCACGTGAAGCTCTGCTGAGCTGCCCTCCCTCC	1861
QY	567	LeuGIyValIyVSGInLyLeuIeuuHsTPValSerIleuGIyGIInIProAsnAla	586
Db	1861	CTGGGGGGTGAAGCANAAGCTTCTGCACCTGGGCTCTCTGTTGGGTCAAGAGCTAAAGCC	1922
QY	587	ThrThrProGIyAspThrIleuAspAlaPheHisCyVleuPheGIuThrGIuAspLySGlu	606
Db	1921	ACCACCCAGAGAGACACCTGGACCCCTTCCACTGCTCTTTGCAAGACTCAAGACAAAGAG	1980
QY	607	PheValAlaGleuAlaIleuAsnSerPheGIInGIuValITrPleuProIIeAsnIInAsnIleu	626
Db	1981	TTTTGTCCCTGGCAATTAAACGGCTTCCAAAGAAAGTGGCTTCCGATTAAACCAAGAACCTG	2044
QY	627	AspIeuIleAlaSerSerPheCyVleuGIInHisCyProCyIleuAspLyValIleArgVal	646
Db	2041	GACTTGATAGCATCTTCTCTCTGCTTCCAGCACTGCTGGATTGCGGAAATTTGGGGTGG	2100
QY	647	AspValIySGIyIlePheProArgAspIuSerAlaGIuAlaCyAspProValaProIeu	666
Db	2101	GATGTCAAAAGGATCTTCCCAAGAGATGATGCTCGGTAGAGCATGTCTGTGGTCCCTCTCA	2166
QY	667	TrpMetArgAspLySerThrIeuIIeGIuGIuGIInTPGIuAspPheCySerMetIeuGIy	686
Db	2161	TGGATGGCGGATTAAGACCTCTCACTTGAAGAGCGTGGAAAGATTTCTGCTCCATGCTTGGCC	2220
QY	687	ThrHisProHisIleuArgGIuIleuAspIleuGIySerSerIleuThrGIuArgAlaMet	706
Db	2221	ACCACCCACACCTCGGACGCTGGACCTGGGACAGAGCATCTTCAAGAGCGGGCCATG	2288
QY	707	LySerThrIeuCyValaIyVleuArgHisProThrCyLyValIeGIInThrIleuMetPheArg	726
Db	2281	AAGACCTGTGTGGCCAGGTGAGCATCCCACTCAAGATACAGACCTGATGTTTAGA	2344
QY	727	AsnAlaGIInIleThrProGIyValaGIInHisIleuTPArgIIeValaMetAlaAsnArgAsn	746
Db	2341	AATGCACAGATTACCCCTGTGTGTGAGCACCTCTGAAGAAATGTGATGGCCCAACGGTAAAC	2400
QY	747	LeuArgSerIleuAsnIleuGIyGIyThrHisIleuLyVSGIuAspValArgMetAlaCyS	766
Db	2401	CTTAAGTCCCTCAACTTGGAGAGGCCACCCACTGAAGAGAAAGAGATGTAAAGATGGCGGTG	2466
QY	767	GIuAlaIleuLyHisAspProLySeyIleuIeuGIuSerIleuArgIleuAspCySeyGIyIleu	786
Db	2461	GAAAGCTTAAACACCCCAAAATGTTGTGTGAGGTCTTGAAGGCTGATGCTGTGTGATTG	2522
QY	787	ThrHisAlaCyVTrpIleuLyValIeSerGIInIleuThrThrSerProSerIleuLySer	806
Db	2521	ACCCTAGCTGTATTACTGAAGATCTCCAAATCTTTAGCACTCCCAAGCCTGAAATCT	2588
QY	807	LeuSerIleuAlaGIyAsnLyValaIhrArgGIInGIyValaMetProIleuSerAspAlaIleu	826
Db	2581	CTGAGCCTGGGAGAAACAAGGTGACAGACCAAGGAGTAATGCTCTCACTATATCCTTG	2644
QY	827	ArgValSerGIInCyValaIeGIInLyVleuIleIeuGIuAspCySGIyIIethrAlaThr	846
Db	2641	AGAGCTCCCAAGTGGCCCTGCAAGAACTGAAATCTGAAGAGATGTGGCATCAACCAAG	2700
QY	847	GIyCySGInSerIleuAlaSerAlaIeuValaSerAsnArgSerIleuThrHisIleuCyVleu	866
Db	2701	GGTGGCCAGAGCTGGGCTCAGCCCTCGTCAGCAACCGGAGCTTACACACTGTGGCTTA	2766
QY	867	SerIleuAsnSerIleuGIyAsnGIuLyValaIleuIleuCyVArgSerMetArgIleuPro	886
Db	2761	TCCACAACAAGCTGGGAGAACAAAGTGTAAATCTACTGTGTCAATCCATAGAGGCTTCCC	2822
QY	887	HisCySerIleuGIuArgIleuMetIleuAsnGIInCyHisIleuAspThrAlaGIyCySGIy	906
Db	2821	CACGTATATCTGCAAGGCTGATGTGTGAATCAAGTGCACACTGCAGACAGGCTGGCTGTGGT	2888
QY	907	PheIeuAlaIleuAlaIleuMetGIyAsnSerTrpIleuThrHisIleuSerIleuSerMetAsn	926

Db	2881	TTTCTTGCACTTGGCCCTTAATGGCTAATGCTGACCACTGAGCCTTACATGAAAC	294
QY	927	ProValGluAspAsnGlyValIysLeuLeuCySGluValMetArgGluProSerCySHs	946
Db	2941	CCTGTGAAGAACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAAACCATCTTGTCAT	3000
QY	947	LeuGlnAspLeuGlnLeuValIysCySHsIleuThrAlaAlaCySGluuSerLeuSer	966
Db	3001	CTCCAGGAGACCTGGAAATGGTGTAAAGTCAATCTCCACCGCGCGTGTGAGACCTGTCC	3060
QY	967	CysValIleSerArgSerArgHisIleuLysSerLeuAspLeuThrAspAsnAlaLeuGly	986
Db	3061	TGTGTGATCTCCAGGAGCAGACACTGAAGAGCTTGAACTTCAACGAGCAATGCTTGAGT	3120
QY	987	AspGlyGlyValAlaAlaLeuCySGluGlyLeuLysGlnLysAsnSerValIleuThrArg	1000
Db	3121	GACGGTGGGGTGGCTGCACTGTGCGCAGGAGCATGAAGCAAAAGAACAGTGTTCAGACAGA	3180
QY	1007	LeuGlyLeuLysValIleCySGlyLeuThrSerAspCySGluAlaLeuSerLeuAlaLeu	1020
Db	3181	CTGGGGTTGAAGGCAATGTGAGCATGTGATTCGATGTGTGAGGCACTCTCTTGGGCCCTT	3240
QY	1027	SerCyAsnArgHisIleuThrSerLeuAsnLeuValGlnAsnAspHisSerProLysGly	1040
Db	3241	TCTTCACACCGGCATCTGACAGCTTAACTGTGTCAGAAATTAATTCAGTCCCAAGGA	3300
QY	1047	MetMetLysLeuCySerSerAlaPheAlaCySProThrSerAsnLeuGlnIleIleGlyLeu	1060
Db	3301	ATGATGAAGCTGTGTGTGGCCCTTGGCTGTCTCCACAGCTTAACTTAAGATTAATGGGCTG	3360
QY	1067	TrpLysTrpGlnTrpProValGlnIleArgGlyLeuLeuGlnGluValGlnLeuLeuLys	1080
Db	3361	TGGAAATGGCAGTACCTCTGTGCNAATTAAGGAAGCTGCTGAGGAAATGGCAGCTAATCAAG	3420
QY	1087	ProArgValIleAlaAspGlySerTrpHisSerPheAspGluAspAspArgHis	1104
Db	3421	CCCCAGATGTAATTAAGCAGGTAATGGCAATCTTTGATGAAGATGACCGGTTAC	3474
RESULT 5			
US-10-860-761-3			
; Sequence 3, Application US/10860761			
; Publication NO. US20040248775A1			
; GENERAL INFORMATION:			
; APPLICANT: WETH			
; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS			
; FILE REFERENCE: AM.01318			
; CURRENT APPLICATION NUMBER: US/10/860,761			
; CURRENT FILING DATE: 2004-06-03			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 3			
; LENGTH: 3885			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURES:			
; NAME/KEY: CDS			
; LOCATION: (1)..(3603)			
US-10-860-761-3			
Alignment Scores:			
Pred. No.: 0			
Score: 5741.50			
Percent Similarity: 96.16%			
Best Local Similarity: 95.90%			
Query Match: 81.16%			
Db:	18	Indels: 41	Gaps: 1
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QY	1	MetGluGlyAspLeuSerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGlu	20
Db	154	ATGGAAGAGAGACAAATTCGCTCACTTTTCCAGCTACGGGCTGCATAGAGTCTCTATGAG	213

QY 21 LeuApLySGIUGIUPheGINThrPheLYSGIULeuLYSLYSSerSerGIUSer 40
Db 214 CTAGACAAGAGAAATTTACAGACATTCAAGAAATTACAAAGAAATCTTCAGAAATCG 273
QY 41 ThrThrCysSerIleProGINPheGINIleGIUAsnAlaAsnValAGIUCysLeuAlaLeu 60
Db 274 ACCACAGCTTATTTCACAGTTTGAAATCGAAGATGCCACAGTGGAAATGCTGGCACTC 333
QY 61 LeuLeuHISGIUITYrGIYAlaSerLeuAlaTPAlaThrSerIleSerIlePheGIU 80
Db 334 CTTTGATGAGTATATAGAGACATCGCTGGCTAGCTCATTAAGCATTTGAA 393
QY 81 AsnMetAsnLeuAqTThrLeuSerGIULYAlaArgAspMetLYSLYS----- 97
Db 394 AACATGAACCTGCCAACCTCTCGAGAGAGGACAGGATGACATGAAGAACATTCAACA 453
QY 97 ----- 97
Db 454 GAAGATCCTGAAGCAAGATGACCTGACCAAGAACCAAGAAAGTCCAGAAATT 513
QY 98 -----IleSer 99
Db 514 TCACAGCTGTGCAACAAGATAGTCCACAGCTGCAGAGACAAAGAAAGCAAGAAATTTCA 573
QY 100 GlnAlaMetGIUGIUGIYAlaThrAlaAlaGIUThrGIUGIUGIUIleSerGIU 119
Db 574 CAACGTAATGAAACAAGAGGTGCCACAGACAGACAGAAAGAACAAATTTCAACA 633
QY 120 AlaMetGIUGIUGIYAlaThrAlaAlaGIUThrGIUGIUGIUGIYHISGIYAlaAsp 139
Db 634 GCTATGGAACAAGAGGTGCCACAGACAGACAGAAAGAACAAAGCATGGAGGTGAC 693
QY 140 ThrTPAspTYrLYSerHISValMetThrLYSPheAlaGIUGIUGIUAAspValArgArg 159
Db 694 ACAATGGAGCTACAAAGATCACTGATATGCAAAATTCGCTAGAGAGAGATGTAAGTGT 753
QY 160 SerPheGIUAsnThrAlaAlaAspTPProGIUwecGINThrLeuAlaGIYAlaPheAsp 179
Db 754 AGTTTGAACACCTGCTGCTGACGTGGCCGGAATGCAACGTGGCTGTTCCTTTGAT 813
QY 180 SerAspArgTPArgLYPheArgProArgThrValValLeuHISGIYLYSSerGIU 199
Db 814 TCACACGGATGGGCTTCGGGCTGCCAGGATGTTCTGCACGAAAGTCAAGAAATTTGG 873
QY 200 LYSerAlaLeuAlaArgArgIleValLeuCYSTrPAlaGINGIYGIYLeuTYrGINGIY 219
Db 874 AAATCGGCTCTAGCAGAGAGATGCTGTGCTGGGCGCAAGGTGACCTTACCAAGGA 933
QY 220 MetPheSerTYrValPhePheLeuProValArgGIUwecGINArgLYSLYSGIUSerSer 239
Db 934 ATGTCTCTCTACGTCCTTCTCTCCCGTTAGAGATGACAGCGGAAGAGAGAGACGT 993
QY 240 ValThrGIUHeIIeSerArgGIUTrProAspSerGINAlaProValThrGIUUIleMet 259
Db 994 GTCCACAGATTCATCTCCAGAGAGGTGCCACAGCTCCAGGCTCGGTACGGAATCATG 1053
QY 260 SerArgProGIUAArgLYLeuPheIleIleAspGIYPheAspAspLeuGIYSerValLeu 279
Db 1054 TCCCGACCAAGAAAGGCTGTCTTCTCATCTACCGTTTCATGACCTGGGGCTCTGTCTC 1113
QY 280 AsnAsnAspThrLYSLYLeuCYLYAspTPAlaGIUYSGINProProPheThrLeuIle 299
Db 1114 AACCATGACACAAAGCTCTGCAGAAAGCTGGCTGAGAGAGCAGCTCCGTTCACTCATTA 1173
QY 300 ArgSerLeuLeuAqLYValLeuLeuLeuProGIUAspPheLeuIleValThrValArgAsp 319
Db 1174 CGCAGTCTGTGAGAGAGGTCTCTCTCTGATGCTTCTCGATCGTCAACGTCAGAGAC 1233
QY 320 ValGIYThrGIULYSLYLeuSerGIUValValSerProArgTYrLeuLeuValArgGIY 339
Db 1234 GTGGGCAAGAGAGCTCAAGTCAAGAGTCTGTCTCTCCCGTTTACCTGTTAGTAGAGA 1293

QY 340 ILeSerGIYGINIUGIARGIleHISLeuLeuLeuGIUAArgIYIleGIYGINIleGINLYS 359
Db 1294 ATCTCCGGGGAACAAGAAATCCATTGCTCTTGAAGCGAGATGGTGAAGCATCAAG 1353
QY 360 ThrGINIYLeuArgAlaIleMetAsnAsnArgGIUleuLeuAspGINCysGINValPro 379
Db 1354 ACACAAAGGTTCGTGGATCATCAACAAACCGTGAAGTGTCTCAACAGTCCAGGTGCC 1413
QY 380 AlaValGIYSerLeuIleCYValAlaLeuGINLeuGINAspValValGIYGIUSerVal 399
Db 1414 GCCGTGGGCTCTCATCTCGTGGCCCTGACGTGCAGAGACGTGTGGGGGAGACGCTC 1473
QY 400 AlaProPheAsnGINThrLeuThrGINLYLeuHISAlaIlePheValPheHISGINLeuThr 419
Db 1474 GCCCTTTCAACCAAGCTCACAGGCTGCAGCGCTGTACGCGCTTTGGCTTTCATCAGTCA 1533
QY 420 ProArgGIYValValArgArgCYSLYAsnLeuGINIUGIUAArgValValLeuLYAspPhe 439
Db 1534 CTTGAGGCGGTGTCCGGCCCTGTCTCACTTGGAGAAAGATTTCTGMAAGCGCTTC 1593
QY 440 CysArgMetAlaValGIUGIYValTPAsnArgLYSSerValPheAspGIYAspAspLeu 459
Db 1594 TGCGTATGGCTGTGAGAGGAGTGTGAATAGAAATGCAATGATTGATTGATGGTACACCTC 1653
QY 460 MetValGINIYLeuGIYGIUSerGIULeuArgAlaLeuPheHISMetAsnIleLeuLeu 479
Db 1654 ATGGTTCAAGACCTGGGAGGTCTGAGCTCGGTCTGTGTTCAATGAACATCTTCTC 1713
QY 480 ProAspSerHISCYSGIUGIUYrTYrThrPhePheHISLeuSerLeuGINAspPheCys 499
Db 1714 CCAAGACGCCATGTGAGAGTACTACCTTTCTTCACTCTGACTCCAGACTTGT 1773
QY 500 AlaAlaLeuTYrTYrValLeuGINIUGIYLeuGINIleGIUProAlaLeuCYSProLeuTYr 519
Db 1774 GCGGCTTTGACTACGTTAGAGGCGCTGAAATGAGCAAGCAAGCTCTGCCCTGTAC 1833
QY 520 ValGIULYThrLYAspArgSerMetGIULeuLYSGIAlaGIYLeuHISIleHISerLeu 539
Db 1834 GTTGAGAAACAAGAGGTCTCATGAGCTTAAACAGGACAGCTTCAATATCCACTGCTT 1893
QY 540 TrpMetLYAspPheLeuPheGIYLeuValSerGIUAspValArgArgProLeuGIUVal 559
Db 1894 TGGATGAGCGCTTCTTGTGTGGCTCTGTAGCGAAGACCTTAAAGAGGCCATCGAGGTC 1953
QY 560 LeuLeuGIYCYSProValProLeuGIYValLYSGIULYLeuLeuHISrTPValSerLeu 579
Db 1954 CTGCTGGGCTGTCCCGTTCCTCGGGGTGAAGACAAAGCTTCTGCACGTGGTCTCTG 2013
QY 580 LeuGIYGINIProAlaAlaThrThrProGIYAspThrLeuAspAlaPheHISCYSLYLeu 599
Db 2014 TTTGGTCAGAGCTTAATGCCACACCCACAGAGACACCTTGACGCTTCCACTGTCTT 2073
QY 600 PheGIUThrGINAspLYSGIUPheValArgLeuAlaLeuAsnSerPheGINIUGIUAITrP 619
Db 2074 TTTGAGACTCAAGACAAAGATTTGTTGCTTGGCATTTAAACAGCTTCAAGAAATGTGG 2133
QY 620 LeuProIleAsnGINAsnLeuAspLeuIleAlaSerSerPheCYSLYLeuGINHISCYSPro 639
Db 2134 CTTTCCGATTAAACAAGACCTGACTGTGATAGCATCTTCTTCTGCGCTCCAGCACTGTCCG 2193
QY 640 TYrLeuArgLYSLYLeuArgValAspValLYSGIYIlePheProArgArgIUSerAlaGIU 659
Db 2194 TATTTGCGGAAATTCGGGTGATGTCCAAAGGATCTTCCCAAGATGATGTCCGCTGAG 2253
QY 660 AlaCySProValProLeuTrpMetArgAspLYSerThrLeuIleGIUGIUGIINTPGLU 679
Db 2254 GCATGCTCTGTGGCTCTATGATGAGCGGATTAAGACCTCTCATTTGAGAGACGTGGAAA 2313
QY 680 AspPheCYSerMetLeuGIYThrHISProHISLeuLYArgGINLeuAspLeuGIYSerSer 699
Db 2314 GATTTCTGCTCCATGCTTGACCCACCCACACACTGTGGGAGGTGACCTGGGAGACAGC 2373
QY 700 IleLeuThrGIUArgAlaMetLYSerThrLeuCYAlaLYLeuArgHISProThrCYSLYS 719

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Db      2274 ATCCGACAGACCGGCATGAAAGACCTGTGTGCAAGCTGAGGACATCCCACTGCAAG 2433
Qy      720  ILGGINThLeuMePheArgAsnAlaGlnIleThrProGlyValGlnHisLeuThrArg 739
Db      2434 ATACAGACCCCTGATGTTTGAAGAAATGACAGATATCCCTGTGTGCAACACTCTGTGAGA 2493
Qy      740  ILLeValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuArgGlu 759
Db      2494 ATCTGATGCGCCACCCGTAACCTTAAGATCCCTCAACTTGGAGGACCCCACTGAAGAA 2553
Qy      760  GluArgValArgMetAlaCysGlnAlaLeuArgHisProArgCysLeuLeuGlnSerLeu 779
Db      2554 GAGGATGAAAGATGCGCTGTGAAGCCTTAAACACCCCAAAATGTTTGTGGAGCTTTG 2613
Qy      780  ArgLeuArgProCysGlyLeuThrHisAlaCysGlyLeuLeuArgHisSerGlnIleLeuThr 799
Db      2614 AGGCTGATGCTGTGAGATGACCCATGCTGTGTAACCTGAAGATCTCCCAAAATCTTACG 2673
Qy      800  ThrSerProSerLeuLeuSerLeuSerLeuArgIleAsnArgValThrAspGlnGlyVal 819
Db      2674 ACCCTCCCAAGCTGAATCTCTGAGCCTGTGCAAGAAACAGGTACACAGACCGGAGTA 2733
Qy      820  MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLeuLeuIleLeuGlu 839
Db      2734 ACGCTCTCAGATGATGCTTGAAGGCTCTCCAGTGCGCCCTGCAAGACTGATACCTGAG 2793
Qy      840  AspArgGlyIleThrAlaIleThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db      2794 GACTGTGATCATCACAGCCAGGTTGCAAGATCTGGGCTCAGCCCTGTGCAAGACCGG 2853
Qy      860  SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyValAsnGlnGlyValAsnLeu 879
Db      2854 AGCTTGACACACCTGTGCTTATTCACACACAGCTTGGGAAACAGAGTGTAATTTACTG 2913
Qy      880  CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db      2914 TGTGATCATGAGGCTTCCCACTGTAGTCTGCAAGAGGCTGATCTGAATCAGTGCAC 2973
Qy      900  LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
Db      2974 CTGACACAGGCTGTGTGTCTCTTCTTCACTTGTGCTTAAATGAGTACATGAGCTGAG 3033
Qy      920  HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuCysGlnVal 939
Db      3034 CACCTGAGCCTTAGATACCCCTGTGAAGACATGCGTAAGCTTCTGTGCGAGGCTC 3093
Qy      940  MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValIleCysHisLeuThrAla 959
Db      3094 ATGAGAGAACATCTTGTCAATCTCCAGGACCTGAGATTGTTAAAGTGTCACTCACCC 3153
Qy      960  AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLeuSerLeuAsp 979
Db      3154 GCGGTGCTGTGAGAGCTCTCTCTGTGTGATCTCGAGAGACAGACACTGAAGAGCCTG 3213
Qy      980  LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuLeuGln 999
Db      3214 CTCACGAGCAATGCGCTGTGAGCGGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3273
Qy      1000  LysAsnSerValLeuThrArgLeuGlyLeuArgValCysGlyLeuThrSerAspCysCys 1019
Db      3274 AAGAAACAGTGTCTGACAGAGACTCGGAGTTGAAGGATGTGAGACTGACTTGTGATG 3333
Qy      1020  GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db      3334 GAGGACACTCTCTTGTGCGCTTCTGCAACCGGCACTGACCAAGCTTAACCTGTGTGAG 3393
Qy      1040  AsnAsnProSerProCysGlyMetCysLeuCysSerAlaPheAlaCysProThrSer 1059
Db      3394 AATAACTTCACTGCCAAGAAATGATGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3453
Qy      1060  AsnLeuGlnIleIleGlyLeuTrpArgTrpGlnTrpProValGlnIleArgIleLeu 1079

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Db      3454 AACTTACAGATTAATTTGGCTGTGAAATGCAATACCTGTGTCAAAATAGAAAGCTGTG 3513
Qy      1080  GluGluValGlnLeuLeuLeuProArgValIleLeuArgIleSerTrpHisSerPheAsp 1099
Db      3514 GAGGAGTGCAGACTTCTAAGCCCGAGTCTTAATGACGTAAGTGTGGCATTTCTTTGAT 3573
Qy      1100  GluAspAspArgHis 1104
Db      3574 GAAGATGACCGGTAC 3588

RESULT 6
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US2004002669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2003-04-16
; CURRENT APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 56.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 17 Gaps: 1

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Qy      21  LeuAspLeuGluGluPheGlnThrPheLeuGluLeuLeuGlyGlySerSerGluSer 40
Db      214  CTAGCAAGAGAAATTTCAACATTCAGAAATTAAGAAATTAAGAAATTTCAAGAAATCG 273
Qy      41  ThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db      274  ACCACATGCTCTAATTCACAGTTTGAAATGCAAGATGCCAACGTGGAATGTGTGCACTC 333
Qy      61  LeuLeuHisGluTrpTrpGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db      334  CTCTTGATGATGATTAATGAGAGATCGCTGCGCTGAGTACATGATGATGATGATGAA 393
Qy      81  AsnMetAsnLeuArgTrpLeuSerGlyValAlaArgAspAspMetCysGly----- 97
Db      394  AACATGAACCTGCCAACCTCTCGAGAGAGCACGGATGACATGAAAGAAACATTCACCA 453
Qy      97  ----- 97

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Dh 454 GAAGATCTGAAGCAGATGACTGACCAAGAGCCAGAAAGAAAAAGTCCAGGAATT 513
Qy 98 -----1eser 99
Dh 514 TCACAGCTGTGCACAAAGATAGTGTCCACAGCTGCAGAGACAAAGAAAGAAATTTCA 573
Qy 100 GlnAlaMetGluGluGluGluValAlaThrAlaAlaGluThrGluGluGluGluIleSerGln 119
Dh 574 CAACCTATGGAACAAAGAAAGGTGTCCACAGCACAGAGACAGAAAGAAATTTTCAAA 633
Qy 120 AlaMetGluGluGluGluValAlaThrAlaAlaGluThrGluGluGluGluValIleGluValAsp 139
Dh 634 GCTATGGAACAAAGAAAGGTGTCCACAGCACAGAGACAGAAAGAAAGGTGTAC 693
Qy 140 ThrTrpAspTyrIleYsSerHisValMetThrIleYsPheAlaGluGluGluValAspValArgArg 159
Dh 694 ACAATGGAGCTACAGAGAGTCACTGATGACCAAAATTCGTGAGAGAGAGATGACGTCTGT 753
Qy 160 SerPheGluAsnThrAlaAlaAspTrpProGluMetGluThrLeuAlaGluValAlaPheAsp 179
Dh 754 AGTTTGAAGAACACTGCTGTGACTGTGACCGGAAATGCAACGTTGTGCTGTGAT 813
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Dh 814 TCACACCGGTGGGCTTCGAGCTTCGACGAGTGTTCGACAGAAAGTCAAGAAATTTGGG 873
Qy 200 LysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGluGluGluYleuYrGluGlu 219
Dh 874 AAATCGGCTTACGACAGAGAGATCTGTGTCTGTGGGCAAGGTGACCTTACAGAGGA 933
Qy 220 MetPheSerTyrValPhePheLeuProValArgGluMetGluArgYleYsGluSerSer 239
Dh 934 ATGTTCTCTACGCTTCTCTCCCGGTAGAGAGATGACGCGGAAAGAAAGAGAGCAGT 993
Qy 240 ValThrGluPheIleSerArgGluThrProAspSerGlnAlaProValThrGluIleMet 259
Dh 994 GTCCAGAGTTCATCTCCAGAGAGTGCAGACCTCCAGGCTCCGAGTACAGAAATTCATG 1053
Qy 260 SerArgProGluArgLeuPheIleIleAspGluPheAspAspLeuGluSerValLeu 279
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Dh 1114 AACATGACACAAAGCTCTGCACAAAGACTGGCTGAGGAGCCTCCCTTCACTCATTA 1173
Qy 300 ArgSerLeuLeuArgYleValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319
Dh 1174 CGCAGTCTGTGAGGAGAGTCTGTCTCCCTGAGTCTTCTGATCTGACCGTCAAGAGAC 1233
Qy 320 ValGluThrGluYleYsLeuYsSerGluValAlaSerProArgTyrLeuLeuValArgGlu 339
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Qy 340 IleSerGluGluGluGluGluIleHisLeuLeuLeuGluArgGluYleGluGluHisGluYs 359
Dh 1294 ATCTCCGGGAAACAAAGAAATCACTTGTCTTGAAGCGGAGATGGGACATCAGAAAG 1353
Qy 360 ThrGluGluLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGluValPro 379
Dh 1354 ACACAAAGGTTGTGCGATCATCAACAAACGTGAGCTGCACCACTGACAGGTGCC 1413
Qy 380 AlaValGluSerLeuIleCysValAlaLeuGluLeuGluAspValAlaGluYleYsSerVal 399
Dh 1414 GCCGTGGGCTCTCTCATCTGCTGTGCTTCGAGCTGCAGAGACGTGTGTGGGAGAGAGCTC 1473
Qy 400 AlaProPheAsnGluThrLeuThrGluYleuHisAlaAlaPheValPheHisGluLeuThr 419
Dh 1474 GCCCCTTTCAACCAAGCTCAAGGCTGCAGGCTGTTCGCTTTTGGGCTTTCACTAGTCAAC 1533
Qy 420 ProArgGluValValArgArgCysLeuAsnLeuGluGluArgValValLeuYsArgPhe 439

Dh 1534 CTTGAGCGCTGTGTCCGCGCTGTCTCAATCTGAGAGAAAGATTGTCTGAGCGCTTC 1593
Qy 440 CysArgMetAlaValGluGluValTrpAsnArgYsSerValPheAspGluAspAspLeu 459
Dh 1594 TGCCGTATGGCTGTGAGAGGAGTGTGAATAGAAATCAGATGTTGATGGTGAAGACCTTC 1653
Qy 460 MetValGluGluYleuGluYleuSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
Dh 1654 ATGGTTCAAGGACTGGGAGAGTGTGAGCTCGTGTCTGTTTCAAGAAATCTTCTTC 1713
Qy 480 ProAspSerHisCysGluGluYrTyrThrPhePheHisLeuSerLeuGluAspPheCys 499
Dh 1714 CCACACAGCCACTGTGAGAGTACTACACTTCTTCCACTCTGACTCTCCAGAGCTTCTGT 1773
Qy 500 AlaAlaLeuYrTyrValLeuGluGluYleuGluIleGluProAlaLeuCysProLeuYr 519
Dh 1774 GCCCCTTTGATCACTGATTAGAGGGCTGTGAATTCAGACCAAGCTCTGTGCCCTGTGAC 1833
Qy 520 ValGluYsThrIleYsArgSerMetGluLeuYleGluAlaGluPheHisGluHisSerLeu 539
Dh 1834 GTTGAGAAACAAAGAGTCCATGAGCTTAAACAGCAGGCTTCCATATCCACTCGCTT 1893
Qy 540 TrpMetIleYsArgPheLeuPheGluYleuValSerGluAspValArgAspProLeuGluVal 559
Dh 1894 TGGATGAAGCTTCTTGTGTGCTGTGAGCGAAGACGTAAAGAGGCCACTGAGAGTCC 1953
Qy 560 LeuLeuGluYsProValProLeuGluValYsGluYsLeuLeuHisTrpValSerLeu 579
Dh 1954 CTGCTGGGCTGTCCCGTTCCCTGGGGGTGAAGCAGAAAGCTTGTGACTGGGTCTCTCTG 2013
Qy 580 LeuGluYleGluGlnProAsnAlaThrThrProGluYsAspThrLeuAspAlaPheHisCysLeu 599
Dh 2014 TTGGGTCAAGCAGCTTAATGCAACACCCAGAGAACCTTCGACGCTTCCACTGTCTT 2073
Qy 600 PheGluThrGluAspYsGluPheValArgLeuAlaLeuAsnSerPheGluGluValTrp 619
Dh 2074 TTCAGACTCAAGCAAGAGATTGTTCGCTTGGCACTTAAACAGCTTCCAGAAAGTGTGG 2133
Qy 620 LeuProIleAsnGluAsnLeuAspLeuIleAlaSerSerPheCysLeuGluHisCysPro 639
Dh 2134 CTTCGATTAACCAAGACCTGGACTTGATAGCATCTTCTGTCTCCAGACAGTGTCCG 2193
Qy 640 TyrLeuArgYsIleArgValAspValIleGluYlePheProArgAspGluSerAlaGlu 659
Dh 2194 TATTTGGGAAATTCGGGTGTGATGCAGAGGATCTTCCCAAGATGATGCTCGCTGAG 2253
Qy 660 AlaCysProValValProLeuTrpMetArgAspYsThrLeuIleGluGluGlnTrpGlu 679
Dh 2254 GCATGTCTGTGTGCTCTATGAGATCGGGAATGACCTCTCATTTGAGAGAGTGGGAA 2313
Qy 680 AspPheCysSerMetLeuGluYrThrHisProHisValuArgGluLeuAspLeuGluSerSer 699
Dh 2314 GATTTCTGTCTCATGCTTTGGACCCACCACTGTGGGAGGTGAGACTGTGGAGCAGC 2373
Qy 700 IleLeuThrGluArgAlaMetYsThrLeuCysAlaYsLeuArgHisProThrCysYs 719
Dh 2374 ATCTGACAGAGCGGGCATGAGACCTGTGTGCAAGCTGAGAGCTCCACCTGCAAG 2433
Qy 720 IleGluThrLeuMetPheArgAsnAlaGluIleThrProGluValGluHisValLeuTrpArg 739
Dh 2434 ATACAGACCTCTGATTTTAAATGACACAGTTTACCTCTGTGTGTGCAACCTTGGAGA 2493
Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluYleYrThrHisLeuYsGlu 759
Dh 2494 ATCTCATGGGCAACCGTTAACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAAGAA 2553
Qy 760 GluAspValArgMetAlaCysGluAlaLeuYsHisProYsCysLeuLeuGluSerLeu 779
Dh 2554 GAGGATGTAAGATGCGGTGAAGCCTTAAACACCAAAATGTTGTGAGTCTTTG 2613
Qy 780 ArgLeuAspCysCysGluYleuThrHisAlaCysThrYsLeuYsIleSerGlnIleLeuThr 799
Dh 2614 AGGCTGAATGTGTGATGATGACCATGCTGTTACTGAAGATCTCCAAATCTTACG 2673

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QY 800 ThSerProSerLeuLYSerLeuSerLeuAlaGlyAlaSerValThrAspGlnGlyVal 819
Db 2674 ACCTCCCCCACTGAAATCTCTGAGCTGGAGAGAAACAAGTACAGACAGGAGGAT 2733
QY 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLYLeuGln 839
Db 2734 ACGCTCTCAGTGAAGCTTGGAGGCTCTCCAGTCCGCTGCAAGACTGATCTGAG 2793
QY 840 AspCysGlyLeuThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db 2794 GACTGTGCATCAACAGCCAGGAGTGGCCAGAGTCTGGGCTCAAGCCCTGTCAAGACCG 2853
QY 860 SerLeuThrAlaLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeu 879
Db 2854 AGCTTGACACACCTGTGCTTACCAACAAGCCTGGGGAAGCAAGGTAAATCTACTG 2913
QY 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db 2914 TGTGCATCAAGAGGCTTCCCACTGTAGTCTGCAGAGGCTGATCTGAATCAAGTGCAC 2973
QY 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuMetGlyAsnSerThrLeuThr 919
Db 2974 CTGACACAGGCTGGCTGTGCTTCTTCTGCACTTGGCTTATGGCTTCAATGGCTGACG 3033
QY 920 HisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValLYLeuLeuCysGlyVal 939
Db 3034 CACCTGACCTTATGATTAACCTCTGGAAGCAATGCGGTGAAGCTTCTGTGCAAGTTC 3093
QY 940 MetArgGlnProSerCysHisLeuGlnAspLeuGlnValLYCysHisLeuThrAla 959
Db 3094 ATGAGAGAACCATCTTGTCACTCTCCAGGACCTGAGGTGGTAAAGTGCATCTCAACGCC 3153
QY 960 AlaCysCysGlySerLeuSerCysValIleSerArgSerArgHisLeuLYSerLeuAsp 979
Db 3154 GCGGTCTGTGAGAGTCTCTGTGTATCTCGAAGACAGACACCTTGAAGAGCTGTGAT 3213
QY 980 LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlyLYLeuLYGln 999
Db 3214 CTCACGACAAATGCCCTGGGTGACGAGTGGGTGCTGCGCTGTGCAAGGACCTGAAGCA 3273
QY 1000 LYAsnSerValLeuThrArgLeuGlyLeuLYAsnLYCysGlyLeuThrSerAspCys 1019
Db 3274 AAGAACAAGTGTTCGAGAGACTGGGTGAAGGATGTGAGACTGACTTCTGATTGCGT 3333
QY 1020 GlnAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db 3334 GAGGCACTCTCTGCGCTTCTGCAACCGGCACTGACCAAGTCTAAACCTGGTGCAG 3393
QY 1040 AsnAsnProSerProLYMetMetLYLeuCysSerAlaPheAlaCysProThrSer 1059
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QY 1060 AsnLeuGlnIleLeuLYLeuThrLYSerGlnTYrProValGlnIleArgLYLeuLeu 1079
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QY 1080 GlnGlnValGlnLeuLeuLYProArgValIleAspGlySerThrHisSerPheAsp 1099
Db 3514 GAGGAGAGGCGAGTCAAGACCCCGAGTGCATTAATGAGTGAATGCGATTCTTTGAT 3573
QY 1100 GlnAspAspArgHis 1104
Db 3574 GAAAGATGACCGGTAC 3588

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RESULT 7
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication NO. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services

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; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 96.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
Gaps: 1

US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)

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QY 21 LeuAspLYGlnGluPheGlnThrPheLYGlnLeuLeuLYLYSerSerGlnLYSer 40
Db 214 CTAGACAGAGAAATTTTCAACATTCAGAAATTTACTTAAGAAATTTCTTCAAGATCG 273
QY 41 ThrThrCysSerIleProGlnPheGlnIleGlnAsnAlaAsnValGlnCysLeuAlaLeu 60
Db 274 ACCACATCTCTATTTCCACATTTGAATGAGATGCAAGTGAATGTCTGGCACTC 333
QY 61 LeuLeuHisGlyTYrTYrGlyAlaSerLeuAlaTPAlaThrSerIleSerIlePheGln 80
Db 334 CTCTTGATGATGATTAATGAGATCGCTGCGCTGAGCTCATGATTCATTCATTGAA 393
QY 81 AsnMetAsnLeuArgTYrThrLeuSerGlnLYAsnArgAspMetLYLeu----- 97
Db 394 AACATGAACCTGCAACCTCTCGAAGAGGACGAGTGAATGAAGAAACATTCAACCA 453
QY 97 ----- 97
Db 454 GAAATCTTGAAGCAAGATGATGACCAAGACCAAGCAAGAAAGTCCAGGAT 513
QY 98 -----IleSer 99
Db 514 TCACAAGTGTGCAACAAGATAGTGCACAGCTGCAGACAAAGAAAGCAAGAAATTTCA 573
QY 100 GlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnIleSerGln 119
Db 574 CAACTATGAAACAAGAGGTGCAACGACAGACAGACAGAAAGAAATTTCAACA 633
QY 120 AlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnIleGlyLYAsp 139
Db 634 GCTATGAAACAAGAGGTGCAACGACAGACAGACAGAAAGAAACAGACATGAGGTAC 693
QY 140 ThrTPAspTYrLYSerHisValMetThrLYPheAlaGlnGlnGlnAspValArgArg 159
Db 694 ACATGAGCTACAAAGATGACGATGATGACCAATTCCTGCTGAGGAGATGTACGTCGT 753

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QY 160 SerPheGluuEntThrAlaAlaSerTrpProGluuMetGlnThrLeuAlaGlyValaPheAsp 179
Db AGTTTGAACACCTGCTGCTGACGGCCGGAATGCAACGTTGGCGTGGCTTTTAT 813
QY 180 SerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyTleGly 199
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QY 200 LysSerAlaLeuAlaArgArgTleValLeuGlySerTrpAlaGlnGlyGlyLeuTrgGlnGly 219
Db AAATCGGCTTAGCCAGAAAGATCGTGTGCTGGGGGCAAGGTGACCTTACAGGGA 933
QY 220 MetPheSerTrpValaPhePheLeuProValaArgGluMetGlnaGlyLysGlnSerSer 239
Db ATGTTCTCTCAAGCTTCTTCTCCCTGTAGAGAGATGACGGGAAGAGAGAGAGAGCT 993
QY 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259
Db GTCAAGATTCATCTCAGGGAGTGGCCAGACCTCCAGGCTCCGGTGAACGAGATCATG 1053
QY 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279
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QY 280 AsnAsnAspThrLysLeuGlyLysAspTrpAlaGlyLysGlnProPheThrLeuIle 299
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QY 300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValaArgAsp 319
Db CGAGTCTGTGAGAGAGCTGTGTCTCCCTAGTCTTCTGATCTGTACCGTCAAGAAC 1233
QY 320 ValGlyThrGluLysLeuLysSerGluValaSerProArgTrpLeuLeuValaArgGly 339
Db GTGGGACAGAGAAAGCTCAAGTCAAGAGTCCGATCTCCCGTTACCTTTAGTTAGAGA 1293
QY 340 IleSerGlyGlnGlnArgIleHisIleLeuLeuGluGluArgGlyIleGlyGlnHisGlnLys 359
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QY 360 ThrGlnGlyLeuArgGlyAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValaPro 379
Db ACACAAAGGATGGCGGATCATCAACAAACGTGAGCTGCTGACCAAGTGCAGAGTGGCC 1413
QY 380 AlaValGlySerLeuIleCysValaAlaLeuGlnLeuGlnAspValaValGlyLysSerVal 399
Db GCCGTGGGCTCTCATCTGCGTGGCCCTGACGTCGACGACGTGTGGGGAGAGGCTC 1473
QY 400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419
Db GCCCCCTTCAACCAACGCTCAGAGGCTGACCGCGCTTTTGGCGTTTCATCAGCTCAC 1533
QY 420 ProArgGlyValaValaArgArgCysLeuAsnLeuGlnGluArgValaValLeuLysArgPhe 439
Db CCTGAGGCGGTGTCGGCGGCTGTCTCATCTGAGAGAAAGATTGCTTCAACGCGCTTC 1593
QY 440 CysArgMetAlaValaGlnGlyValaTrpAsnArgLysSerValaPheAspGlyAspAspLeu 459
Db TGGCGTATGCTGTGAGAGAGTGTGAAATAGAAAGTCAAGTGTGATGAGTGAAGGACTC 1653
QY 460 MetValGlnGlyLeuGlyGlySerGlyLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
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QY 480 ProAspSerHisCysGlnGluTrpTrpThrPhePheHisLeuSerLeuGlnAspPheCys 499
Db CGAGCAAGCCACTGAGAGAGTACTACACTTCTTCCACTCAAGTCTCAAGAACTTCTGT 1773
QY 500 AlaAlaLeuTrpTrpValaLeuGlnGlyLeuGlnIleGlnProAlaLeuCysProLeuTrp 519
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QY 520 ValGluLysThrLysArgSerMetCysLeuLysGlnAlaGlyPheHisIleHisSerLeu 539

Db 1834 GTTAGAAGACAAAGAGCTCCATGAGCTTAAACAGGACAGGCTTTCATATTCATCTCCTT 1893
QY 540 TrpMetLysArgPheLeuPheGlyLeuValaSerGluAspValaArgArgProLeuGluVala 559
Db TGGATGAAGGCTTCTGTTTGGCTCTGTAGAGGAAACGTTAAGAGAGCCACTGAGAGTC 1953
QY 560 LeuLeuGlyCysProValaProLeuGlyValaLysGlnLysLeuLeuHisGlyTrpValaSerLeu 579
Db CTGCTGGGCTGTCCCGTTCCTCGGGGGTGAAGAGAAAGCTTCTGCACTGGGTCTCTCTG 2013
QY 580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
Db TTGGGTGAGGACCTTAATGCCACCAACAGAGACACCTTGACGCGCTTCCACTGTGCTT 2073
QY 600 PheGluThrGlnAspLysGlnPheValaArgLeuAlaLeuAsnSerPheGlnGluValaTrp 619
Db TTCCAGACTCAAGACAAAGATTTGTTCCGCTTGGCATTAACGCTTCCAAAGAGTGTGG 2133
QY 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
Db CTTCGATTAAACAGAACTGGAAGTGTATGATGATCTTCTTGTGCTCCAGCACTGTCCG 2193
QY 640 TyrLeuArgLysIleArgValaAspValaLysGlyTlePheProArgAspGlyLysSerAlaGlu 659
Db TATTGGGAAATTCGGGTGAGTCAAAAGGATCTTCCAAAGATGAGTCCGCTGAG 2253
QY 660 AlaCysProValaValaProLeuTrpMetArgAspLysThrLeuIleGlnGlnGlnTrpGlu 679
Db GCATGCTCTGTGCTCCCTCTATGGAATCGGGATGAAGACCTCATTTAGAGAGAGTGGAA 2313
QY 680 AspPheCysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySerSer 699
Db GATTTCTGCTTCAAGCTTGGCACCCACCACTGGGAGGCTGAGCACTGGGACAGAGC 2373
QY 700 IleLeuThrGlnArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719
Db ATCTGACAGAGCGGGCATGAAGACCTGTGTGCAAGCTGAGAGCTCCACCTGTGAG 2433
QY 720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValaGlnHisIleuTrpArg 739
Db ATACAGACCTCTGATGTTTAAAGATGACACAGATTAACCTCTGTGTGCAACCTCTGAGA 2493
QY 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisIleuLysGln 759
Db ATCGTATGGGCAACCGTAACCTTAAGATCCCTTCACTTGGAGGCAACCACTTAAGAA 2553
QY 760 GluAspValaArgMetAlaCysGlnAlaLeuLysHisProLysCysLeuLeuGlnSerLeu 779
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QY 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysEtyrLeuLysIleSerGlnIleLeuThr 799
Db AGGCTGAATGCTGTGAATTTGAACCATGCTGTGTAACCTGAAGATCTCCAAATCTTAA 2673
QY 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValaThrAspGlnGlyVala 819
Db ACCTCCCGCAAGCCGAAATCTGAGCTGGCAGGAAACAAAGTGAACAGACGAGGAGTA 2733
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QY 860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValaAsnLeuLeu 879
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Db 2914 TGTGATCATGAGGCTTCCCACTGATCTGACAGGCTGATCTGATCATGAGCCAC 2973
Qy LeuapThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
Db 2974 CTGACACGGCTGGCTGGTCTTCTTGGACTTGGCTTAAAGGAACTCATGGCTGACG 3033
Qy HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuLeuCysGluVal 939
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Qy 940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValIleCysHisLeuThrAla 959
Db 3094 ATGAGAGAACCATCTTGCATCTCCAGACCTGAGAGTGGTAAAGTGCATCTCACCCCC 3153
Qy 960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLeuSerLeuSer 979
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Qy 980 LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGluGlyLeuLeuValGln 999
Db 3214 CTCACGACATGCCCCCTGGGTGACGGTGGCTGCTGGCTGTGGAGGACTGAAGCA 3273
Qy 1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
Db 3274 AAGAACAGTGTCTGACGAGACTCGGGTGAAGCATGTGACCTGATTTGCTGT 3333
Qy 1020 GluAlaLeuSerLeuAlaLeuSerCysAspAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db 3334 GAGGACCTCTCTTGGCCCTTCTCGCAACCGGCACTGACGATCAACCTGTGTGACG 3393
Qy 1040 AsnAspHisSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
Db 3394 AATACTTCACTGCTCCAAAGAAATGAAAGCTGTGTGGCTTGGCTTGCCTCCACGCT 3453
Qy 1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeu 1079
Db 3454 AACTTACGATATATGGCTGTGGAAATGGCAGTACCTGTGCAATGAAGAAGCTGTG 3513
Qy 1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099
Db 3514 GAGGAAGGCAAGTACTCAAGCCCGAGTGGTAAATGACGATGTGCAATCTTTGAT 3573
Qy 1100 GluAspAspArgHis 1104
Db 3574 GAAAGTACCCGCTAC 3588

RESULT 8
US-10-216-645-3
Sequence 3, Application US/10216645
Publication No. US20030125282A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
APPLICANT: LESSL, MONIKA
APPLICANT: PETERS-KOTTIG, MICHAEL
APPLICANT: BECKMANN, GREGOR
TITLE OF INVENTION: HUMAN MATER PROTEINS
FILE REFERENCES: SCH-1910
CURRENT APPLICATION NUMBER: US/10/216, 645
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 101 39 874, 3 1
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 3830
TYPE: DNA
ORGANISM: Homo sapiens
US-10-216-645-3

Alignment Scores:
Pred. No.: 0 Length: 3830
Score: 5683.50 Matches: 1087
Percent Similarity: 95.87% Conservative: 5

Best Local Similarity: 95.43% Mismatches: 12
Query Match: 80.34% Indels: 35
DB: 15 Gaps: 2
US-10-066-521-6 (1-1344) x US-10-216-645-3 (1-3830)

Qy 1 MetGluGlyAspLysSerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGlu 20
Db 1 ATGGAGAGAGACAAATGCTCTACCTTTCCAGCTACGGGGCTGCAATGGGTCTCATGAG 60
Qy 21 LeuAspLysGluGluPheGlnThrPheLysGlyLeuLeuLysLysLysSerLysSer 40
Db 61 CTAGCAAGAGAAATTTCAACATTTCAAGCAATTAATTAAGAAATTTCCAGAAATCG 120
Qy 41 ThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db 121 ACCAATGCTCTAATTCACAGTTGAATTCAGAAATGCAACGTTGAATGTCTGACATC 180
Qy 61 LeuLeuHisGluTrpTrpGlyValAserLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db 181 CTCTTGATGATGATTAATGAGCATCGCTGGCTGGCTAGTTCATTAAGCATCTTTGAA 240
Qy 81 AsnMetAsnLeuArgThrLeuSerGlyLysAlaArgAspAspMetLysLysIleSerGln 100
Db 241 AACATGAACCTGCCAACCTCTCGAGAAAGGACCGAGTGAATGAAATAATTCACCAAG 300
Qy 101 -----AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGln--- 115
Db 301 GATCTGAAGCAACGATGATGACCAAGAACCAAGCAAGAAAGTCCAGAAATTA 360
Qy 115 ----- 115
Db 361 TATGCAATGACTAAGCTTATCTTGGGGGTCTGACATCTGACTCGAATTAATAACAC 420
Qy 116 -----GluIleSerGlnAlaMetGluGlnGly 125
Db 421 AAGTATGTGAATTCATTTCTTTTCGCAAAATTTCAAGCTATGAACAAGAAAGT 480
Qy 126 AlaThrAlaAlaGluThrGluGlnGlnIleIleGlyLysAspTrpTrpAspTrpLysSer 145
Db 481 GCCACAGACAGACAGACAGAAACAGAGATGAGGTGACATGTGGACTTCAAGAGT 540
Qy 146 HisValMetThrLysPheAlaGluGluLysAspValArgAspSerPheGluAsnThrAla 165
Db 541 CACGTGATGACCAATTCGCTGAGAGAGAGATGATCTGATTTGAAACATCTCT 600
Qy 166 AlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpLysPhe 185
Db 601 GCTGCTGGCCGGAATGCAAAAGTGGCTGTGCTTTGATTCAGACCGGTGGGGCTTC 660
Qy 186 ArgProArgThrValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 205
Db 661 CGGCTCGCAGGGTGTCTGACAGAAAGTCAAGAAATGGGAATCGCTCTGAGCCGA 720
Qy 206 ArgIleValLeuCysTrpAlaGlnGlyLeuTrpGlnGlyMetPheSerTrpValPhe 225
Db 721 AGAATCGTGTCTGGCCGCAAGGTGACTTACAGGGAATGTTCTCTACGCTTC 780
Qy 226 PheLeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSer 245
Db 781 TTCCTCCCGTTAAGAGATGCAAGGAAAGAAAGAGACATGTCACAGATTCATCTCC 840
Qy 246 ArgGluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeu 265
Db 841 AGGAGTGGCCAGACTCCAGGCTCCGCTGACGAGATCAAGTCCCGACCAAGAAAGGCTG 900
Qy 266 LeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeu 285
Db 901 TTGTTCACTTGAAGGTTTGATGACCTGGGCTGTGCTCCACAAATGACCAAGCTC 960
Qy 286 CysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLys 305
Db 961 TGCAAAAGCTGGGCTGAGAGACACCTCCGTTACCTGCATACCGCATGCTGCTAGAGAG 1020

QY 306 ValLeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeu 325
Db 1021 GTCCGCTCCCTGAGTCTTCTGATCGTCAACCGTCAGAGAGCGGGCAGAGAGAGCTC 1080
QY 326 LysSerGluValValSerProArgTyrLeuLeuValAlaArgIYIleSerGlyGluAlaArg 345
Db 1081 AAGTCAAGAGGTGGTGTCCCGCTTAACTGTAGTTAAGGAATCTCCGGGGAAACAAAGA 1140
QY 346 IleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAla 365
Db 1141 ATCCACTTGCTCTTGAAGCGGGGATTTGGTGAAGATCAGAAAGACAAAGAGTTGCTGCG 1200
QY 366 IleMetAsnAsnArgIYIleLeuLysArgGlnCysGlnValProAlaValGlySerLeuIle 385
Db 1201 ATCATGAACAAACCGGAGCTCTCGACAGTGCAGCGGCGCGGTGGGCTCTCTCATC 1260
QY 386 CysValAlaLeuGluLysGluAspValValGlyGluSerValAlaProPheAsnGlnThr 405
Db 1261 TGCCTGGCCCTGCAGCTGCAGAGACGTGGTGGAGAGAGCGTGCCTTCAACCAACG 1320
QY 406 LeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValAlaArg 425
Db 1321 CTCACAGGCTGCAGCGCGCTTTGTGTTCATCAGCTCACCCCTCAGAGGCTGTCGG 1380
QY 426 ArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGlu 445
Db 1381 CGCTGTCTCAATCTGAGAAAGAGTTGCTCTGAAAGCGCTTCTGCGGTATGGCTGTGAG 1440
QY 446 GlyValITrPasnArgLysSerValPheAspGlyAspPheMetValGlnGlyLeuGly 465
Db 1441 GGAGTGTGAATAGAGAGTCAAGTGTTCACGTGACGATGCTCATGTTCAGAGACTCGGG 1500
QY 466 GluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGlu 485
Db 1501 GAGTGTGAGTCCGTGCTCTGTTCATGAACATCTTCTCCAGAGACCACTGTAG 1560
QY 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
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QY 506 LeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArg 525
Db 1621 TTAGGGGCTGTGAATGAGACAGCTCTGCGCTGTGACTGTGAAGAACAAAGAGG 1680
QY 526 SerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyrMetLysArgPheLeu 545
Db 1681 TCCATGAGCTTAAACAGGACGCTTCCATTCACCTGCTTGGATGAAGCGTTTCTTG 1740
QY 546 PheGlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProVal 565
Db 1741 TTTGGCCTCGTGAAGAGAGAGTGAAGGCGCATGAGGTCCTGCTGGGCTGCCCTT 1800
QY 566 ProLeuGlyValLysGlnLysLeuLeuHisIleTrpValSerLeuLeuGlyGlnGlnProAsn 585
Db 1801 CCCCTGGGGGTGAAGCAAGAGCTTCTGCACTGGGTCTCTGTGGGTGCACAGGCTTAAT 1860
QY 586 AlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLys 605
Db 1861 GCCACCAACCAAGAGACACCTTGAGCGCTTCCACTGCTTTTTCGAACCTCAAGACAA 1920
QY 606 GluPheValArgLeuAlaLeuAsnSerPheGlnGluValITrPLeuProIleAsnGlnAsn 625
Db 1921 GAGTTTGTTCGCTTGGCATTAACAGCTTCCAGAAAGTGGCTTCCGATTAACAGAAC 1980
QY 626 LeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArg 645
Db 1981 CTGGACTGATAGCATCTTCTTCTGCTCCAGCACTGTCCGTAATTTTCGGAAAAATTGG 2040
QY 646 ValAspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValPro 665
Db 2041 GTGATGTCAAGGAGATCTTCCCAAGAGATGATGCTGCGTGAAGCATGTCTGTGCTCCT 2100

QY 666 LeuITrMetArgAspLysThrLeuIleGluGluGlnITrProLysAspPheCysSerMetLeu 685
Db 2101 CTATGATGGGGGATTAAGACCTCATTTAGAGAGAGAGGAGAAATTTCTCTCATATCTT 2160
QY 686 GlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla 705
Db 2161 GGCACCAACCAACCTTGGCGAGCTGAACTGGAGCGAGCATCTTCAAGATACAGACCTGAT 2220
QY 706 MetLysThrLeuCysAlaLysLeuArgHisProThrCysAlaIleGlnThrLeuMetPhe 725
Db 2221 ATGAAGACCTGTGTGCAAGCTGAGCATCCCACTGCAAGATACAGACCTGATGTTT 2280
QY 726 ArgAsnAlaGlnIleThrProGlyValGlnHisLeuITrParGlyIleValMetAlaAsnArg 745
Db 2281 AGAATATCAAGATTAACCTGTGTGTACACACTCTGAGAAATCGTCATAGGCCAACCT 2340
QY 746 AsnLeuArgSerLeuAsnLeuGlyIleThrHisIleuLysGluGluAspValArgMetAla 765
Db 2341 AACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAAGAGAGATGTAAAGATGGCG 2400
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Db 2401 TGTGAAGCTTTAAACACCCAAATGTTGTGTGAGCTTTGAAGCTGATTTGCTGTGGA 2460
QY 786 LeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLys 805
Db 2461 TTGACCCATGCTGTACTTGAAGATCTCCCAATCTTACAGACTCCCAAGCTTAAA 2520
QY 806 SerLeuSerLeuAlaGlyAsnLysValIThrAspGlnGlyValMetProLysSerAspAla 825
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QY 826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAla 845
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QY 846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865
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QY 866 LeuSerAsnAsnSerLeuGluLysGluGlyValAlaAsnLeuCysArgSerMetArgLeu 885
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QY 886 ProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisIleuAspITrAlaGlyCys 905
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QY 906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerITrLeuThrHisIleuSerLeuSerMet 925
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QY 926 AspProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCys 945
Db 2881 AACCTTGAAGACAATGGGTGTAACCTTGTGCGAAGGTCAAGAGAAACCAATCTTGT 2940
QY 946 HisLeuGlnAspLeuGluLeuValLysCysHisIleuThrAlaAlaCysCysGluSerLeu 965
Db 2941 CATCTCGAGACCTGAGGATTGGTAAAGTTCATCTCACCGCGGCTCTGTAGAGCTG 3000
QY 966 SerCysValIleSerArgSerArgHisIleuLysSerLeuAspLeuITrAspAsnAlaLeu 985
Db 3001 TCTGTGTGATCTCGAGAGAGACACTGTAAGGCTGTGATTCACGAGCAATGCCCTG 3060
QY 986 GlyAspGlyGlyValAlaAlaAlaLeuCysGluGlyLysLeuLysGlnLysAsnSerValLeuThr 1005
Db 3061 GGTACCGGTGGGTGTGTGCACTGTGGAAGGAACTGAAGCAAAAGAACAGTGTCTGACG 3120
QY 1006 ArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAla 1025
Db 3121 AGACTCGGGTTGAAGGCAATGGAATACTTGTGATTTGCTGTGAGGCACTCTCTTGGCC 3180
QY 1026 LeuSerCysAsnArgHisIleuThrSerLeuAsnLeuValGluAsnAsnPheSerProLys 1045

Db 833 GTCTCCCGTTACTGTTAGTAAAGAAATCTCCGGGAACAAAGAAATCACTTGCTCTCT 892
Qy 350 uGluAArglyIleGlyGluHisGlnLeuThrGlnGlyLeuArgAlaIleMetAaanaar 370
Db 893 TGAACGCGGAGATGGTGAGCATCAAGAAACAAGAGGTTCGTGCATCAAGAAACAACCG 952
Qy 370 ggGluLeuLeuAaArgIleCysGlnValProAlaValGlySerLeuIleCysValAlaLeuG 390
Db 953 TGAACTGCTCAACCAAGTGCAGAGTGCCTGCGTGGGCTCTCTCAATGCGTGGCCCTGCA 1012
Qy 390 nLeuGlnAaArgValAlaGlyGluSerValAlaProPheAaGlnIleThrLeuThrGlyLeuHis 410
Db 1013 GCTGCAAGAACCTGGTGGGGAGAGAGTGCCTCCCTTCAACCAAGCTCAAGGCTTGCA 1072
Qy 410 sAlaAlaPheValPheHisGlnLeuThrProArgGlyValValAlaArgArgCysAaanaIle 430
Db 1073 CGCGCTTTGTTGTTTCATCAAGCTCAACCTCGAAGGCGTGGTCCGGCGCTGTCTCAATCT 1132
Qy 430 uGluGluAArgValAlaLeuLeuYsaArgPheCysArgMetAlaValGluGlyValIlePheAaArg 450
Db 1133 GAGAGAAAGAGTGTCTCGAAGCGCTTCTGCGTATGGCTGTGAGAGGAGTGTGAATAG 1192
Qy 450 gLySerSerValPheAaArgIleAaAaPheLeuMetValGlnGlyLeuGlyGluSerGluLeuArg 470
Db 1193 GAAGTCAAGTGTTCAGCGGTGACGACCTCATAGTTCAAGAGACTCGGGAGAGTCTGAGCTCG 1252
Qy 470 gAlaLeuPheHisMetAaanaIleLeuLeuProAaSerHisCysGlnGluIleYrYrThrPh 490
Db 1253 TGCTGTGTTTCATCAATGAACATCTTCTCCAGACGACCTGTGAGAGGAGTCAACCTT 1312
Qy 490 ePheHisAaLeuSerLeuGlnAaPhePheCysAlaAlaLeuYrYrYrYrYrYrYrYrYrYrYr 510
Db 1313 CTTCACCTCAAGTCTCCAGAGACTTCTGTGCGCTTGTACTAAGCTTGAAGAGGCGCTGGA 1372
Qy 510 uIleGlnProAlaLeuCysProLeuYrYrValGlnIleYrThrYsaArgSerMetGluLeuLeu 530
Db 1373 AATGAGGCAAGCTCTTGCTCCCTCTGTACGTTGAGAAAGCAAGAGGCTCAAGAGCTTAA 1432
Qy 530 sGlnAlaGlyPheHisAlaIleHisSerLeuYrPheMetYsaArgPheLeuPheGlyLeuValIse 550
Db 1433 ACAGGCAAGGCTTCCATATCACTCGCTTGTGATGAAGGTTTCTTGTGGCTCGTAG 1492
Qy 550 rGluAaArgValAlaArgArgProLeuGlnValLeuLeuGlyCysAaProValProLeuGlyValIly 570
Db 1493 CGAAGACGTAAAGAGGCACTGAGAGTCTCTGTGGCTGTGCCGTCTCCCTGGAGGAGTAA 1552
Qy 570 sGlnIleLeuLeuHisIleYrValIleSerLeuLeuGlyGlnGlnProAaAlaThrProG 590
Db 1553 GCAAGAGCTTCTGCACTGGGTCTCTGTGGGTCAAGAGCTTAATGCCACCAACCCAGG 1612
Qy 590 yAaPThrLeuAaArgAlaPheHisCysAaLeuPheGlnIleThrGlnAaPheGlyGluPheValArgle 610
Db 1613 AGACACCTTGACGCGCTTCCACTGTCTTTCGAGCTCAAGACAAGAGTTTGTTCGCTT 1672
Qy 610 uAlaLeuAaAaSerPheGlnGlnIleValIlePheProIleAaGlnIleAaLeuAaPheIleAl 630
Db 1673 GGCATTAAACAGCTTCCAAAGAGTGTGCTTCCATTAAACCAAGAACCTGAGATTGAATAGC 1732
Qy 630 aSerSerPheCysLeuGlnHisCysProYrYrLeuArgYrYrIleArgValAaPheValIlySG 650
Db 1733 ATCTTCCTTCTGCTCCAGCACTGTCCGTAATTTGCGAAGAAATTCGGGTGAAATGTCMAAG 1792
Qy 650 yIlePheProAArgAaArgIleSerAlaGlnAlaCysAaProValAlaProLeuYrPheAaArg 670
Db 1793 GATCTTCCCAAGAGATGAGTCCGCTGAGGCAATGTCCTGTGCTCATAGATGCCGGA 1852
Qy 670 pLySerThrLeuIleGluGluGlnIlePheGluAaPheCysSerMetLeuGlyThrHisProHis 690
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Qy 690 sLeuAaArgIleAaPheLeuGlySerSerIleLeuThrGlnAaArgAlaMetYrYrThrLeuY 710
Db 1913 CTTGCGGAGCTGAGCTGGGACAGATCTCTGACAGAGCGGCGCATGAAGACCTGTGTG 1972

Qy 710 sAlaIleLeuAaArgHisAaProThrCysAlyIleGlnIleThrLeuMetPheAaArgAaAlaGlnIle 730
Db 1973 TGCCAAAGCTAGAGATCTCCACTGCAAGATACAGACCTGATGTTTGAATGACAGAT 2032
Qy 730 eThrProGlyValGlnHisLeuThrPArgIleValMetAlaAaAaArgAaLeuAaArgSerle 750
Db 2033 TACCTTGATGTGAGCACTCTGAGAAATGTCATGAGCCCAACCGTAACCTTAAGATCTCT 2092
Qy 750 uAaLeuGlyGlyYrThrHisLeuYsaGlnGluAaPheValArgMetAlaCysGlnAlaLeuLeu 770
Db 2093 CAATCTGGAGGACCCACCTGAAAGAAAGATGTAAAGATGGCGTGTGAAGCTTAA 2152
Qy 770 sHisProYsaCysLeuLeuGluSerLeuAaGluAaPheCysGlyLeuThrHisAlaCys 790
Db 2153 ACACCCAAATGTTTGTGTGAGATCTTGAAGGCTGGATGTGCTGTGATTAAGCCATGCTG 2212
Qy 790 sYrYrLeuYsaIleSerGlnIleLeuThrYrYrSerProSerLeuYsaSerLeuSerleuAl 810
Db 2213 TTACTGAAGATCTCCAAATCTTACAGACCTCCCGAGCTGAATCTCTGAAGCTTGGC 2272
Qy 810 aGlyAaAaLeuValThrAaArgIleValMetProLeuSerAaPheAlaLeuAaArgValIserG 830
Db 2273 AGAAACAAGGTGACAGACCGGAGATATGCTCTCAGTGAATGCTTGAAGATCTCCA 2332
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Db 2333 GTGCGCCCTCGAAGAGCTGATACCTGAGAGACTGTGGCATCAACCGAGGTTCGAGAG 2392
Qy 850 rLeuAlaSerAlaLeuValIserAaAaArgSerLeuThrHisAaLeuCysAaLeuSerAaAaAse 870
Db 2393 TCTGGCTCAAGCTCTGTCAGCAACCGAGACTTGAACACCTGTGCTTAACAACAAG 2452
Qy 870 rLeuGlyAaGlnGluValAaLeuLeuCysAaArgSerMetArgLeuProHisCysSerle 890
Db 2453 CTGGGGAACAAGGTTAATATCTACTGTGTCAATCATAGAGTTCCCACTGTATCTT 2512
Qy 890 uGlnAaArgLeuMetLeuAaGlnCysHisAaLeuAaPThrAlaGlyCysGlyPheLeuAlaI 910
Db 2513 GCAAGAGCTGATGTGATGATGACGACCTGACACAGCGGTGGCTGTGTGTTCTTGCACT 2572
Qy 910 uAlaAaLeuMetGlyAaAaSerTrpLeuThrHisAaLeuSerLeuSerMetAaProValGluAa 930
Db 2573 TGCGCTTATGGATACCTCATGAGCTGAGACGACCTGAAGCTTATGATGAACCTGTGGAAGA 2632
Qy 930 pAaGlnValIleLeuLeuCysGlnValMetAaArgIleProSerCysHisAaLeuAaPhe 950
Db 2633 CAATGGCGTGAAGCTTCTGTGCCAGATCATGAAGAACATCTTGTCACTCCAGAGACT 2692
Qy 950 uGluLeuValIlyCysHisAaLeuThrAlaAlaCysCysGluSerLeuSerCysValIleIse 970
Db 2693 GAGATTGTGAAGTGCATATCAACCGCGGTGCTGTGAAGATCTGTCTGTGTGATCTC 2752
Qy 970 rArgSerArgHisAaLeuYsaSerLeuAaPheLeuThrAaAaArgAlaLeuGlyAaPheGlyVal 990
Db 2753 GAGGAGCAAGACCTGAAGAGCTGAGATCTCAAGCAAAAGCCCTGGGTGAACGAGTGGGT 2812
Qy 990 lAlaAlaLeuCysGlnGluIleYsaGlnYsaAaSerValIleThrArgLeuGlyLeuLeu 1010
Db 2813 TGCTGCACTGTGCAAGGAGCTGAAGCAAAAGAACAGTCTTCAAGAGACTCGGGTTGAA 2872
Qy 1010 sAlaCysGlyLeuThrSerAaPheCysGlnAlaLeuSerLeuAlaLeuSerCysAaAaArg 1030
Db 2873 GGCATGTGACTGACTTGTGATGTGTGAGGACTCTCTTGGCCCTTCTGCAACCG 2932
Qy 1030 gHisAaLeuThrSerLeuAaAaLeuValGlnAaAaAaPheSerProYsaGlyMetMetYrIse 1050
Db 2933 GCATCTAACCAAGTCTAAACCTGTGCAAGATTAATCTTCAAGCCCAAGAAATGATGAAGCT 2992
Qy 1050 uCysSerAlaPheAlaCysProThrYrSerAaAaLeuGlnIleGlyLeuYrYrYrYrYrYrYr 1070
Db 2993 GTGTTCCGCTTGTGCTGTCCCAAGTCTTAATTAAGATTAATGGGCTGTGGAATGGCA 3052

QY 1070 nTy-ProValIglInIleArglyLeuLeuGluGluValIglInLeuLeuLysProArgValIva 1090
Db 3053 GTACCTCTGTGAATTAAGAAAGCTGCTGAGGAAAGTCACTCAAGCCCGAGTGT 3112
QY 1090 IILASPGIYserTPHISerPheAspGluAspArgHis 1104
Db 3113 AATGACGGTAGTGGCACTCTTGTGATGAAGATGACCGTAGC 3155

RESULT 10

US-10-399-443-5
Sequence 5, Application US/10399443
Publication No. US2004002869A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary, Department of Health & Human Services, The National Institute
APPLICANT: Health
APPLICANT: Nelson, Lawrence M.
APPLICANT: Tong, Zhi-Bin
APPLICANT: Nelson, Lawrence
APPLICANT: Zhi-Bin, Tong
TITLE OF INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64785
CURRENT APPLICATION NUMBER: US/10/399,443
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/241,510
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 3447
TYPE: DNA
ORGANISM: Mus musculus
US-10-399-443-5

Alignment Scores:

Pred. No.: 8.76e-276 Length: 3447
Score: 2688.00 Matches: 554
Percent Similarity: 66.49% Conservative: 186
Best Local Similarity: 49.78% Mismatches: 293
Query Match: 38.00% Indels: 81
Gaps: 11

US-10-066-521-6 (1-1344) x US-10-399-443-5 (1-3447)

QY 15 GlnTrpCysLeuTyrgIuLeuAspIyGluIupheGlnThrPheLysGluLeuLys 34
Db 163 CAATGGGCTCTCA-GAAAAAGACGTAAAGCAATCTTGAAGACCGTAGTGAAGAG 221
QY 35 LysLysSerSerGluSerThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsn 54
Db 222 GAACAGAGATCAGAAAGCA----- 242
QY 55 ValGluCysLeuAlaLeuLeuLeuHisGluTyrgIyAlaSerLeuAlaTrrAlaThr 74
Db 242 ----- 242
QY 75 SerIleSerIlePheGluAsnMetAsnLeuArgThrIleuSerGluTyrgAlaArgAspArg 94
Db 243 ---ATGCTCTCTTCAAGAAATGTCTAGTAGCAATCTTGAAGACAGATGATCAGAAAGAA 299
QY 95 MetLysLysIleSerGln----- 100
Db 300 GTGAAACAGCGCTCAGAAAGAAATGACTTCTCCAGAAAAGACAGTAATCAATCCAG 359
QY 101 -----AlaMetGluGlnGluGluAlaThrAlaAlaGluThrGluGluGln 115
Db 360 AAAAGACCAAGACAGACAGACAGACAGACATCAGAAACCTTACATCTTAAGAAAGAAAT 419
QY 116 GluIleSerGlnAlaMetGluGlnGluGluAlaThrAlaAlaGluThrGluGluGlnGly 135
Db 420 GAAAGTACAGAGCA-----GATTAAGAT 443

QY 136 HisGlyGlyAspThrTrpAspTyrgLysSerHisValMetThrLysPheAlaGluGlu 155
Db 444 AATGAGGTGACTTAACAAGACTCAAGAGCCATGATGTGTAAGTTGACACAAGGTGTG 503
QY 156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
Db 504 GATCTACAC-----TATGACAGCCAGAGATGAATTAATTAATGCT 542
QY 176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleHisGlyLys 195
Db 543 GATGCTTTTAACCATACCAAGAAACCTTCCAGCTTCAACACATATATCTACAGAAAGA 602
QY 196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGly 215
Db 603 CAGAGAGTGGAGACTAGCTTTGGCCAGAGATTTGTTCTTGGTGGGACAGGTAA 662
QY 216 LeuTyrgInGlyMetPheSerTyrgValPhePheLeuProValArgGluMetGlnArgLys 235
Db 663 CTCTCCAAAAATG---TCTTGTGTCATCTTCTCTGTAGAGAAATTAAGTAGACA 719
QY 236 LysGluSerSerValThrGluPheIleSerArgIuTrpProAspSerGlnAlaProVal 255
Db 720 GAGAAAGACAGTTGGCACAGCTGATGTGAAGAGTGTCCAGACTCTGGAGATCTAGTG 779
QY 256 ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu 275
Db 780 ACAAGATCATCTCCCAACCAAGAAAGCTCTTGTGTGCATAGATGCTTGAGATGTG 839
QY 276 GlySerValLeu---AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnPro 294
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QY 295 ProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIle 314
Db 900 ATATACATCTGATGATGACAGCTCTGAGAAAGCTCTCTTAACCTCACTCTTCTCAATC 959
QY 315 ValThrValArgAspValGlyThrGluLysLeuLysSerGluValValIleSerProArgTyrg 334
Db 960 ATTACACACCAAGAACACAGGCTTGAAGAAATCTCAAGTCAATGTGTGTCCCTCTCAT 1019
QY 335 LeuLeuValArgGlyLysSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyLys 354
Db 1020 ATACTGTTGAAAGAGCTGTGATCAAGAGATCTCAAGCTGATGCTTCAAGAAATCTCC 1079
QY 355 GlyLysIleGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAsp 374
Db 1080 AATGAGCTGATGAATGAATGAAGTCTTCATCTCTGATGAAGAAATCAACAGCTGTTGAC 1139
QY 375 GlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspVal 394
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Db 1200 CTGGGAAGAGATGACCCCTACCTGACAGCTCTACCCGTTTGTATGCCAGCTGTG 1259
QY 415 PheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluArgVal 434
Db 1260 TTTTACACAGCTCACTTGAAGAAAGCCCTTCCAGAGCCCTCACTCACTCAAGAAAGCA 1319
QY 435 ValLeuLysArgPheCysArgMetAlaValGluGluValTrrPanaArgLysSerValPhe 454
Db 1320 ACTCTAGTGGTGTGTGATGATGAGCTGAAGAGAGTGTGAACATGAGAGTGGTGTG 1379
QY 455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
Db 1380 TATATATATATGCTGAAGAACTATAGCTTAAGAGAGTGTAGATCTTGCCCTTTTAC 1439
QY 475 MetAsnIleLeuLeuProAspSerHis---CysGluGluTyrgTyrrPhePheHisLeu 493
Db 1440 ATGAACATCTCTTCCAGGTGGCCACAGACAGTGAAGAGTATATGTTTCTCCACCTC 1499

QY 494 SerLeuGlnAapPheCyAlaAlaLeuTyTyrValLeuGluGluLeu---GluTleGlu 512
Db 1500 AGCTTCGAGGATTTCTTGTGCTCTATATATATGTTTAAAGAGGCTGGAGAAATGGAAT 1559
QY 513 ProAlaLeuCyProLeuTyTyrValGluTyrThrIysArgSerMetGluLeuGlnAla 532
Db 1560 CAGCATTTTTC-----TTCAATGAAAACCAAGAGCATCATGAGGTAAAGAACT 1613
QY 533 GlyPheHisIleHisSerLeuTyrMetIysArgPheLeuPheGlyLeuValSerGluAap 552
Db 1614 GAC---GACACTGCGCTCTCGGAGTGAAGGTTTCTATTTGGCTCATGAACAAGAT 1670
QY 553 ValArgArgProLeuGluValLeuLeuGlyCyProValProLeuGlyValGluGlnIys 572
Db 1671 ATCTGAAGACTCTGGAGGTCTGTTGAATATCCCGGATTCGAATGTCAGTTCAGCAAG 1730
QY 573 LeuLeuHisTyrValSerLeuLeuGlyValGlnGlnProAlaAlaThrThrProGlyAapThr 592
Db 1731 CTCGAACACTGGGCTCTCTCTATAGCTCAGAGGTCAATGGACACCAAGCCCAATGACACC 1790
QY 593 LeuAapAlaPheHisCyAlaLeuPheGluThrGlnAapIysGluPheValArgLeuAlaLeu 612
Db 1791 CTGATGCTCTTATTTGTTCTATTTGAGTCTCAGAGTGAAGATTGTTGGCGGGGCTCTC 1850
QY 613 AapSerPheGlnGluValTyrLeuProIleAapGlnAapLeuAapLeuIleAapSer 632
Db 1851 AAACGCTTCGAAGAGTGTGCTCTGATTTAACCAAGAGATGAGCTTCGAGGCTCTTCC 1910
QY 633 PheCyLeuGlnGlnIleCyProTyrLeuAapIysIleArgValAapValIysGlyIlePhe 652
Db 1911 TACTGTCTCAAGCACTGTCAACAATCTTAAGGCAATCCGGTGGATATATAGACCTCTC 1970
QY 653 ProArgAapGluSerAlaGluAlaCyProValValProLeuTyr---MetArgAapIys 671
Db 1971 TCGAGATATTAATCTCTGAGCTGTGCTGTTGTACTGTCCAGAGACACAAATGTAAAG 2030
QY 672 ThrLeuIleGluGlnTyrGluTyrGluAapPheCySerMetLeuGlyThrIleProHisLeu 691
Db 2031 CCCCTCCATGAGAGTGTGGGAAATCTGTCTGTGTGGCTGGACGCTCCGGAATCTTG 2090
QY 692 ArgGlnLeuAapLeuGlySerSerIleLeuThrGluArgAlaMetIysThrLeuCyAla 711
Db 2091 AAGAGCTGAGCTTGGGAGCAAGCACTCTAGTCAACGGGCAATGAATATCTGTGCTC 2150
QY 712 LysAlaArgHisProThrCyAlaIleGlnThrLeuMetPheArgAapAlaGlnIleThr 731
Db 2151 GAGCTGGGGAATCACTCTCGAACAATACAAAGCGTGAAGCTTTAAGATGCAAGATAGT 2210
QY 732 ProGlyValGlnIleLeuTyrArgIleValMetAlaAapArgAlaLeuArgSerLeuAap 751
Db 2211 TCTGGCTCGAAACATCTCTGGAAGCTCTTTTGTAGCAATCAAACTTAAGTACTCTCAAT 2270
QY 752 LeuGlyGlyThrHisIleLeuGlyGluAapValArgMetAlaCyGluAlaLeuIleHis 771
Db 2271 CTAGAGAACTCCCAATGAAGATGATACATGAAGTTAGCTCGAAGCCCTGAACAT 2330
QY 772 ProLysCyAlaLeuGluSerLeuArgLeuAapCyAlaLeuThrHisAlaCyArgTyr 791
Db 2331 CCAAGTCTCCCGTGAAGACTCTGAGGTGATTCCTGTAGTTAACATCATGTTAT 2390
QY 792 LeuIysIleSerGlnIleLeuThrThrSerProSerLeuIysSerLeuSerLeuAlaGly 811
Db 2391 GAGATGATCTCAGAGCTCTTATTTCAACCAAGGCTAAAGTGTCTCAGCTGCGCCAA 2450
QY 812 AapIysValThrArgGlnGlyValMetProLeuSerAapAlaLeuArgValSerGlnCy 831
Db 2451 AATGAGGGAGATGAAGATATATCCCTGGAGATGCTTGAAGTCAATGCTCAATGTGT 2510
QY 832 AlaLeuGlnIysLeuIleLeuGluAapCyAlaIleThrAlaThrGlyCyGlnSerLeu 851
Db 2511 CTACTGGAAAGATGATCTGACAACTGTGGCTCAACACTGCGCAGTGTCACTTCTG 2570
QY 852 AlaSerAlaLeuValSerAapArgSerLeuThrHisIleLeuCyAlaSerAapAapSerLeu 871

Db 2571 GTCTACGCTCTTTTCAAGAACAGACTTGAACACCTGTGCTGTCAACACAGCTTG 2630
QY 872 GlyAapGluGlyValAapLeuLeuCyArgSerMetArgLeuProHisCySerSerLeuGln 891
Db 2631 GGAAGTGAAGAGTGAAGCAAGCTGTGTCAAGTCTCTGAGAAATCCAGAAATGTGCTCAG 2690
QY 892 ArgLeuMetLeuAapGlnCyHisIleAapThrAlaGlyCyGlyPheLeuAlaLeuAla 911
Db 2691 CGGCTGATTAAGTCACTCAACATTTGATGATGATCTTATGCTTCTCGCAATAGA 2750
QY 912 LeuMetGlyAapSerTyrPheThrHisIleLeuSerSerMetAapProValGluAapAap 931
Db 2751 CTTCGAACACACAAAGCTGACCTGAGCTGACATGAACCCCGTAAAGGGAGTGT 2810
QY 932 GlyValIysLeuLeuCyGluValMetArgGluProSerCyHisIleGlnAapLeuGln 951
Db 2811 GCATGAAGTCACTGTGTGAAGCTTTAAGAAACCTACTTTTACCTTCAAGAACTGGA 2870
QY 952 LeuValIysCyHisIleThrAlaAlaCyCyGluSerLeuSerCyValIleSerArg 971
Db 2871 CTAGTGACTGCGCAACTCACAAGACTGCTGCGAGGACCTGTATGATCACAACA 2930
QY 972 SerArgHisIleIysSerLeuAapLeuThrAapAapAlaLeuGlyAapGlyValAla 991
Db 2931 ACCAAGCACTTAAAGCTTGGATCTGTGAACACGCTGGGTGTCAAAGAGTATA 2990
QY 992 AlaLeuCyGluGlyLeuIysGlnIysAapSerValLeuThrArgLeuGlyLeuValAla 1011
Db 2991 ACCCTGTGAAGGACGTGAAGCAAGTACAGCTCCCTGAGAGACTTGGGTTGGGGCA 3050
QY 1012 CyGlyLeuThrSerAapCyCyGluAlaLeuSerLeuAlaLeuSerCyAapAapHis 1031
Db 3051 TGTAAGTGATCTTCAATTCCTGTGAAGCAATGTGCATTTGCTCTTCAACCCCTCAC 3110
QY 1032 LeuThrSerLeuAapLeuValGlnAapAapPheSerProLysGluMetMetIysLeuCy 1051
Db 3111 CTGAACGCTTAAAGCTGGTGAAGATGACTTCAAGTCACTGGGGAATGTAAGCTGTGC 3170
QY 1052 SerAlaPheAlaCyProThrSerAapLeuGlnIleIleGlyLeuTyrIleGlnTyr 1071
Db 3171 TCTGCTTCAATGCTCTGTCTGAACCTGGGATATTTGGCTGTGAAGCAGGATAC 3230
QY 1072 ProValGlnIleArgIysLeuLeuGluGluValGlnLeuLeuIysProArgValValIle 1091
Db 3231 TATCCCGAGTGAAGAACAGCTGGAAGAGTTGATGATCAAGCCCAAGTGTGAT 3290
QY 1092 AapGlySerTyrHisSerPheAapGluAapAapArgHis 1104
Db 3291 GATGATGATTGTATGCTAAGTGAAGATGACCGAAGC 3329

RESULT 11
US-10-677-943--5
Sequence 5, Application US/10677943
Publication No. US20040072297A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
APPLICANT: represented by the Secretary of the Department of Health and
APPLICANT: Human Services
APPLICANT: Nelson, Lawrence
TITLE OF INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64790
CURRENT APPLICATION NUMBER: US/10/677,943
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: 60/241,510
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US02/09776
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2


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; SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-677-943-5

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[illegible]

US-10-066-521-6 (1-1344) X US-10-677-943-5 (1-3447)

[illegible]

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Db 1911 TACTGTCTCAAGCACTGTCAAGCACTTGAAAGCAATCCGGGTGATATCATAGACCTCTC 1970
Qy 653 ProArGaPguSerAlaGluAlaCySPProValProLeuTrp---MetArgAplys 671
Db 1971 TCGAGTAATTAATCTCGAGGTGTGCTGTGTGTACTGTCTCAGAGACACAACTGTAAG 2030
Qy 672 ThrLeuIleGluInuGlnTrpGluAAspPheCySerMetLeuGlyThrHisProHisLeu 691
Db 2031 CCCCTCCATGAGTGTGTGGGAAACTTGTCTGTGTGTGGACCTCCGGAACCTTG 2090
Qy 692 ArgLeuAAspLeuGlySerSerIleLeuThrGluAlaMetLeuThrLeuGlyAla 711
Db 2091 AAGAGCTGAGCTTGGGCGACAGCATCTGTAGTCAACGGGCGATGAATACTGTGCTTC 2150
Qy 712 LysLeuAArgHisProThrCyAlaValIleGlnThrLeuMetPheArgAAspAlaGlnIleThr 731
Db 2151 GAGCTGCGGAATCAAGTCTGCGAATACAGAAAGTGAAGTTTAAGAGCAGAGGTAGTG 2210
Qy 732 ProGlyValGlnHisLeuThrTrpArgIleValMetAlaAspAArgHisLeuAAspSerLeuAsn 751
Db 2211 TCTGCGCTGAACAATCTGTGAAGCTCTTTTATGCAATCAAACTTAAAGTACCTCAT 2270
Qy 752 LeuGlyGlyThrHisLeuLeuGluInuAAspValAArgMetAlaCySGluAlaLeuLysHis 771
Db 2271 CTAGGGAACATCTCCATGAAGATATGATACATGAAGTTAGCTTCCGAAAGCTGAAACAT 2330
Qy 772 ProIyCySLeuLeuGluSerLeuAArgLeuAAspCySGlyLeuThrHisAlaCySTyr 791
Db 2331 CCAAGGTCTCCGTGAGACATCTGAGGTGATTCCTGTGAGTTAACATCATATGGTTAT 2390
Qy 792 LeuLysIleSerGlnIleLeuThrTrpSerProSerLeuLysSerLeuSerLeuAAspGly 811
Db 2391 GAGATGATCTCACCGCTTCTTATTTCAACACAGGCTAAAGTGTCTGACGCTGCGCAA 2450
Qy 812 AsnLysValIThrAAspGlnGlyValMetProLeuSerAAspAlaLeuAArgValSerGlnCyS 831
Db 2451 AATGAGTGGAGATTAAGATATGATATTCCTTGGGAATGCTTGAAGTCAATGATGTGT 2510
Qy 832 AlaLeuGlnLysLeuIleLeuGluAAspCySGlyIleThrAlaThrGlyCySGlnSerLeu 851
Db 2511 CTATGCAAAAGTTGATCTGAGCAACTGTGGCTTCACACCTGACAGCTGCACCTCTTG 2570
Qy 852 AlaSerAlaLeuValSerAAspSerLeuThrHisLeuCySLeuSerAAspAspSerLeu 871
Db 2571 GTCTCAGGCTTTTTCAGAACACAGAACTTGACACACCTGTGCTCAAAACACAGCTGTG 2630
Qy 872 GlyAAspGlnGlyValAAspLeuLeuCyAAspSerMetAArgLeuProHisCySLeuGln 891
Db 2631 GGGAGTGAAGATGTCAACAGCTGTGTCAAGTTCTGAGAAATCCAGAAATGTGCTTCCAG 2690
Qy 892 ArgLeuMetLeuAAspGlnCySHisLeuAAspThrAlaGlyCySGlyPheLeuAlaLeuAla 911
Db 2691 CGGCTGATACTGAATCATCTGCAACTGTGATGATGATGATGATGATGATGATGATGATG 2750
Qy 912 LeuMetGlyAAspSerTrpLeuThrHisLeuSerLeuSerMetAAspProValGluAAspAsn 931
Db 2751 CTTCGAAACACACAAAGCTGACCCACCTGAGCTGACATGAACCCCGTGGAGGATGTGT 2810
Qy 932 GlyValLysLeuLeuCySLeuValMetAArgLysProSerCySHisLeuGlnAAspLeuGlu 951
Db 2811 GCATGAAGCTACTGTGTGAAGCTTTAAAGAACTTACTGTACTTCAAGCTTGAAGAA 2870
Qy 952 LeuValLysCySHisLeuThrAlaAlaCySAspGluSerLeuSerCySValIleSerArg 971
Db 2871 CTATGAGACTGCGCAACTCAACAGAACTGTGCGAGACCTGGCTGTATGATCAACA 2930
Qy 972 SerAArgHisLeuLysSerLeuAAspLeuThrAAspAlaLeuGlyAAspGlyValAla 991
Db 2931 ACCAAGCACTTAAAGATTGTGATCTTGTAAACAACGCTGGGAGCAAAAGAGTCA 2990
Qy 992 AlaLeuCySGlnGlyLeuLysGlnLysAAspSerValLeuThrAArgLeuGlyLeuValAla 1011
Db 2991 ACCGTGTGTGAGGACTGAACAAAGTGAAGCTCCCTGAGAGAGACTTGGGTGGGGCA 3050
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Qy 1012 CySGlyLeuThrSerAAspCySLeuAlaLeuSerLeuAlaLeuSerCySAspAArgHis 1031
Db 3051 TGTAAAGTTAGTACTCCATATGCTGTGAGGCAATGTCAATGCGCATCTCTTGCACACCTTCAC 3110
Qy 1032 LeuThrSerLeuAAspLeuValGlnAAspAAspPheSerProIyGlyMetMetLeuLeuCyS 1051
Db 3111 CTGAACGCTTAAACCTGTGTGAAGAACTTCAAGTCAATCGGGAATGTGAAGCTGTGC 3170
Qy 1052 SerAlaPheAlaCySProThrSerAAspLeuGlnIleIleGlyLeuTrpLysTrpGlnTyr 1071
Db 3171 TCTGCTTCCAAATCCCTGTCTTCACTGAGGATTAATGCTGTGGAAGCAGAGATAC 3230
Qy 1072 ProValGlnIleAArgLysLeuLeuGluGluValGlnLeuLeuLysProAArgValValIle 1091
Db 3231 TATGCCCAAGTGAAGACAGCTGAGAGAGTTGAGTTGTCAAGCCCCACGTGTGAT 3290
Qy 1092 AspGlySerTrpHisSerPheAAspGluAAspAArgHis 1104
Db 3291 GATGATATGTGTATGCTATGATGAAGATGACCGAAAC 3329

RESULT 12
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028694H
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.: 1,466-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)
Qy 252 GlnAlaProValIThrGluIleMetSerAArgProGluAArgLeuPheIleIleAAspGly 271
Db 1 CAAGCTCCGGTGAAGGATCATGTCCGACCAAGAAAGCGCTGTGTTCATCATGAGACGT 60
Qy 272 PheAAspAAspLeuGlySerValIleAAspAAspThrLysLeuCySlysAAspTrpAlaGlu 291
Db 61 TTCATGACTCTGGGCTGTGTCTTCAACATGACACAAAGCTGTGCAGAAAGACTGGGCTGAG 120
Qy 292 LysGlnProProPheThrLeuIleAArgSerLeuLeuAArgLysValIleLeuProGluSer 311
Db 121 AAGCAGCTCGTTCACCTCATATGCGAGTGTGTGAGAAAGTCCGTGCTCCGAGATCC 180
Qy 312 PheLeuIleValIThrValAArgAAspValGlyThrGluLysLeuLysSerGluValValSer 331
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Db 181 TTCCTGATCGTCACCGTCAGAGCGTGGGCAAGAAAGCTCAAGTCAGAGCTGCTCT
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGlyGlnArgIleIleLeuLeuGlu
Db 241 CCCGGTACCTGTTAGTAAGAAATCTCCGGGGAACAAAGAAATCCATGCTCTTGA
Qy 352 ArgGlyIleGlyGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle
Db 301 CGCGGATGCTGAGCATCAAGAAAGGTTGCGTGGATCAATGAACACCTGAG
Qy 372 LeuLeuArgGlnGlyGlnValProAlaValIleSerIleIleCysValAlaLeuGlnLeu
Db 361 CTGCTGACAGAGTCAGAGTCCGCGCTGAGCTCTCATCTGCGGCTGAGCTG
Qy 392 GlnArgValAlaGlyGlnSerValAlaProPheArgGlnIleIleIleIleIleIleIle
Db 421 CAGAGCGTGGGGAAGCGTCCGCTTCAACCAAGCGTCAAGGCGCTGACGCC
Qy 412 AlaPheValPheIleGlnLeuThrProArgGlyValAlaArgArgCysLeuLeuGln
Db 481 GCTTTTGTTTCATCAGCTCAACCCCTGAGGCGTGGTCCGGCGCTGCTCATCTGAG
Qy 432 GlnArgValAlaLeuValArgPheCysArgMetAlaValGlyValIleTrpAsnArgIys
Db 541 GAAAGAGTGTCTGAAAGCGCTTCTGCGGTATGCTGGAAGGAGTGTGAATGGAAG
Qy 452 SerValPheArgGlyAspAspLeuMetValGlnIleGlnIleGlnIleGlnIleGlnIle
Db 601 TCAGGTTTGAAGCGTGAACCTCATGTTCAAGACATCGGGGAGTCAAGCTCGCTCT
Qy 472 LeuPheIleMetAlaIleLeuLeuProAspSerIleCysGlnGlnIleIleIleIleIle
Db 661 CTGTTTCAATGACATCTTCTCCACAGACCACTGAGAACTCATCACTTCTTC
Qy 492 HisLeuSerLeuGlnAspPheCysAlaIleIleIleIleIleIleIleIleIleIle
Db 721 CACCTCAGCTCCAGGACTTCTGTCGCGCTTGTACTAGTGTGAAGGCGCTGAAATC
Qy 512 GlnProAlaLeuCysProLeuTyrValGlnIleIleIleIleIleIleIleIleIle
Db 781 GAGCAGCTCTCTGCTCTGTAAGTGAAGAAAGAGGCTCATGAGGCTTAAACAG
Qy 532 AlaGlyPheIleGlnIleSerLeuIleIleIleIleIleIleIleIleIleIle
Db 841 GAGGCTTCAATCAGCTCTGTTGAATGAAGGCTTCTGTTGCTGCTGAGGCA
Qy 552 AspValArgArgProLeuGlnValIleLeuGlnIleCysProValProLeuGlnValIleGln
Db 901 GACGTAAGAGGCACTGAGGCTCTGCTGGGCTGTCCGTTCCCTGCGGGTGAAGCAG
Qy 572 LysLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db 961 AAGCTTCACTGAGTCTCTGTTGGTCAAGCAGCTAAATGCCACCAAGGAGGAGC
Qy 592 ThrLeuArgAlaPheIleCysLeuPheGlnIleIleIleIleIleIleIleIleIle
Db 1021 ACCCTGAGCGCTTCACTGTTTTCAGACTCAAGCAAGAAATTTGCTGCTTGA
Qy 612 LeuAsnSerPheGlnIleValIleIleIleIleIleIleIleIleIleIleIleIle
Db 1081 TTAACAGCTTCCAAGAGTGTGCTTCCGATTAACAGAACTGGAATTAAGCACT
Qy 632 SerPheCysLeuGln 636
Db 1141 TCCTTCTGCTCAG 1155

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RESULT 13
 US-10-677-943-1
 ; Sequence 1, Application US/10677943
 ; Publication No. US20040072297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America as
 ; represented by the Secretary of the Department of Health and

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; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.: 1,46e-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)
Qy 252 GlnAlaProValThrGlnIleMetSerArgProGlnArgLeuPheIleLeuArgGly 271
Db 1 CAGGCTCGGAGCGAGATATGTCCTCCAGACAAAGAGCTGTTGTTATCATATGACGT 60
Qy 272 PheAspAspLeuGlySerValLeuAsnAsnAspThrIleIleCysValAspTrpAlaGlu 291
Db 61 TTCATGACCTGGGCTGCTGCTCTCAACAAATGACAAAGCTCTGCAAGAGCTGAG 120
Qy 292 LysGlnProProPheThrIleIleIleSerLeuLeuValGlyValLeuProGlnSer 311
Db 121 AAGCAGCTCGGTTCACTCATAGCAGTCTGCTGAGAAAGTCTCTCTGAGTCC 180
Qy 312 PheLeuIleValThrValArgAspValGlyThrGlnIleLeuIleSerGlnValIleSer 331
Db 181 TTCGATGCTGACCGTCAAGAGCGTGGGCAAGAAAGCTCAAGTCAAGGCTGCTCT 240
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGlnArgIleIleLeuLeuGln 351
Db 241 CCCGTTACCTGTTAGTAAGAAATCTCCGGGGAACAAAGAAATCCATGCTCTTGA 300
Qy 352 ArgGlyIleGlyGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 371
Db 301 CGCGGATGCTGAGCATCAAGAAAGGTTGCGTGGATCAATGAACACCTGAG 360
Qy 372 LeuLeuArgGlnGlyGlnValProAlaValIleSerIleIleCysValAlaLeuGlnLeu 391
Db 361 CTGCTGACAGAGTCAGAGTCCGCGCTGAGCTCTCATCTGCGGCTGAGCTG 420
Qy 392 GlnArgValAlaGlyGlnSerValAlaProPheArgGlnIleIleIleIleIleIleIle 411
Db 421 CAGAGCGTGGGGAAGCGTCCGCTTCAACCAAGCGTCAAGGCGCTGACGCC 480
Qy 412 AlaPheValPheIleGlnLeuThrProArgGlyValAlaArgArgCysLeuLeuGln 431
Db 481 GCTTTTGTTTCATCAGCTCAACCCCTGAGGCGTGGTCCGGCGCTGCTCATCTGAG 540
Qy 432 GlnArgValAlaLeuValArgPheCysArgMetAlaValGlyValIleTrpAsnArgIys 451
Db 541 GAAAGAGTGTCTGAAAGCGCTTCTGCGGTATGCTGGAAGGAGTGTGAATGGAAG 600
Qy 452 SerValPheArgGlyAspAspLeuMetValGlnIleGlnIleGlnIleGlnIleGlnIle 471

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Db	601	TCAGGTTGACGGGACGACACTCATTGTTCAAGACTCGGGGAGTCTGACGTCGCGT	660
Qy	472	LeupheH1smeAaSm1leuleuProaapSerH1sCysGluGluTyrTyrThrPhePhe	491
Db	661	CTGTTTCACATGAACATCTCTTCCACAGCACCACTGAGAGGAGTACATCACTCTTC	720
Qy	492	H1sleuSerleuGlnAspPheCysAlaAlaTyrTyrValIleuGluGluIle	511
Db	721	CACCTCAGTCTCCAGGACTTCGTGCGCGCTGTACTGCTTGAAGGGGCTGGAAATC	780
Qy	512	GluProAlaLeuCysProleuTyrValGluTyrThrIlysaGserMetGluLeuIlysgln	531
Db	781	GAGCAGGCTCTCGCCCTCTGTACGTTGAGAGACAAAGAGGCCATGAGCTTTAAACAG	840
Qy	532	AlaGluPheH1s1IleH1sSerleuTyrMetIlysaGPhleuPheGluIlyValIserGlu	551
Db	841	GAGGCTTCATATACACTCGCTTGGATGAAGACGTTCTGTGTGGCCCTCGAGACGAA	900
Qy	552	AspValArgArgProleuGluValIleuLeuGlyCysProValProleuGlyValIlysgln	571
Db	901	GACGTAAAGAGGCCACTGGAGAGTCCGTGGGCTGTGCCGTTCCCTGGGGGGTGAAGCAG	960
Qy	572	IlySleuLeuH1sTyrValIserleuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp	591
Db	961	AAGCTTCGACACTGGGTCTCTCTGTGGGTACAGACCTTAAAGCCACACCCAGAGAGAC	1022
Qy	592	ThrIleuAspAlaPheH1sCysLeuPheGluTyrGlnAspIlyGluPheValArgLeuAla	611
Db	1021	ACCCTGGAGCGCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTGTTCGCTTGGCA	1082
Qy	612	LeuAsnSerPheGlnGluValTyrleuProlIeaGlnAsnIleuAspLeuIleaIaser	631
Db	1081	TTAAACAGCTTCCAGAGAGTGTGGCTTCGATTAAACAGAACTGGAATTGATGATCATCT	1142
Qy	632	SerPheCysIleuGln	636
Db	1141	TCCTTCTGCTCCAG	1155
RESULT 14			
US-10-794-342-2			
: Sequence 2, Application US//10794342			
: Publication No. US20040253615A1			
: GENERAL INFORMATION:			
: APPLICANT: Inohara, Naohiro			
: APPLICANT: Nunez, Gabriel			
: TITLE OF INVENTION: NOD Nucleic Acids and Polypeptides			
: FILE REFERENCE: UM-08922			
: CURRENT APPLICATION NUMBER: US/10/794,342			
: CURRENT FILING DATE: 2004-03-05			
: NUMBER OF SEQ ID NOS: 22			
: SOFTWARE: Patentin version 3.2			
: SEQ ID NO 2			
: LENGTH: 3521			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-10-794-342-2			
Alignment Scores:			
Pred. No.: 5,45e-190			
Score: 1885.50			
Percent Similarity: 56.65%			
Best Local Similarity: 37.95%			
Query Match: 26.65%			
DB: 18			
Gaps: 13			
US-10-066-521-6 (1-1344) x US-10-794-342-2 (1-3521)			

[illegible]

OY	394	ValValIGlUGluserValAlaProhEaenGlnPhtLeuThrGlyLeuGlnIleAlaIaIaPhe	413
Db	1171	GAGAAAGGtGGtGATGTCATGTAAGTCAGCCAAACAACAAGCTGGTTAACTGGCTAT	1233
OY	414	ValPheNIeGlnLeuThrProAlaGlyValValArgGlySerValLeuAlaIleuGlnIaArg	433
Db	1231	ATTCTACCTGGTTGACACCA-----GTAAATGGAAGGCTGCTAACTGTAACCAACCA	1288
OY	434	ValValLeuValArgPheCysArgMetAlaValGlnGlyValIThrAsnArgIleSerVal	453
Db	1285	GCCCAAGCTGAGAAAGACTGGCCAAAGCTGGCCAAAGAAATATGAGATTAAGCTTAAGCTG	1344
OY	454	PheArgIleuArgPheIleuMetValGlnIleuGlyLeuSerGlnIleuArgAlaIePhe	473
Db	1345	TTTTTACAGAAAAATCTCAAGAGGCTGGTTAACTGATCAATGATGATCTGATGTTATG	1406
OY	474	HisMetAsnIleLeuLeuProArgSerHisCysGlnGlyValIThrThePhePheIleu	493
Db	1405	GACAGCAATATTTATTCAGAAAGCAACAAGTATGAAATGCTGTAATGTTACCAACCTT	1466
OY	494	SerLeuGlnIaArgPheCysAlaIaIaLeuIThrValIleuGlnGly---LeuGlnIleGln	512
Db	1465	CATGTTCAGAGCTTTTGTGACAGCTATGTTCTATATGTTGAAGAAAGAGTTGGAACTGGG	1522
OY	513	ProAlaLeuCysProLeuIThr---ValGlnIleValArgSerMetGlnLeuVal	530
Db	1525	AACCTCTCTGCAAGCTTTTGAAATGTAAGTCAATTACTTCAAAAGCAACAATTATAA	1584
OY	531	GlnIaGlnPheNIeIleHisSerLeuIThrMetIleValArgPheIleuPheGlyIleuValSer	550
Db	1585	GATCCC-----CATTTGACACAGAAAGAGCTTTGTGTGGCTTTTGAT	1633
OY	551	GluArgValArgArgProLeuGlnIleValIleuGlnGlyCysProValProLeuGlyValIleu	570
Db	1633	GAAAGTCAAGTAAACATCTGAGAGAGCTTTTAATCTGAAATGCTACAGAAATAA	1692
OY	571	GlnIleValLeuLeuNIeIThrValSerLeuLeuGlnGlnIleProAsnIaIeThrThrProGly	590
Db	1693	TCAAAAGTTACTTCAGTGTATGAGAAATATGGAACAGTACTATCTTCACACAGCTG	1752
OY	591	AspThrIleuAspAlaPheNIeValLeuPheGlnIThrGlnIaArgIleuPheValArgLeu	610
Db	1753	GAATTTCTGAGAGTTGTTCTACCTGTGTATGAGACTCAAGATAAAGCGTTATTAAGCCAG	1812
OY	611	AlaIleuAsnSerPheGlnIleuValIThrProLeuIleAsnGlnIaIleuAspIleuAla	630
Db	1813	GCAATGAGATGTTCCCAAGGTTCCATTAATATTTGTGAAAAATACATTTGGCTGTA	1872
OY	631	SerSerPheCysLeuGlnIleCysProIThrLeuArgIleValLeuValAspValIleuGly	650
Db	1873	TCTTCTTTCTGCTTAAGACATGCGCGAGTGTGGGAGCAATGAGCTGCTGTAACTG	1933
OY	651	IlePheProArgPheIleuSerAlaGlnIaCysProValValProLeuIThrMetArgAsp	670
Db	1933	GTATTTGAGAAAGATATTAATAACAAGCTCCCA---ACTAACTTTGGAGTGGTAT	1988
OY	671	LeuThrIleuIleGlnIleuGlnIThrIleuArgPheCysSerMetLeuGlyThrNIeProHis	690
Db	1990	CGC-----ATTACTCACTGGTTGGGAAGATCTGTGTGGCTTCATTAACAATAAAC	2043
OY	691	LeuArgGlnLeuAspLeuGlnGlySerSerIleuIThrGlnIaGlnIaMetIleuThrLeuCys	710
Db	2044	TTGAGAGAAATGAGCTGTACATGACAACTGATTAATGAGCAATGAAATATCTGGAT	2102
OY	711	AlaIleuValLeuArgNIeSerIThrCysValIleGlnIThrLeuMetPheArgAsnIaGlnIle	730
Db	2104	CATGAACATAAGGCAACCAACCTGTAACTACAAAGAACTACTGTGAATTTATCACTTTC	2163
OY	731	ThrProGlyValGlnIleuIThrArgIleValMetAlaAsnArgAspLeuArgIleu	750
Db	2164	CTGATGGTGTGCAAGATATCTGATCTTTGATGTCAATAAACAATCTGATGCACTT	2222

QY	751	AsnLeuGlyGlyThrHisIleuLysGluGluLysArgValIleAspMetAlaCysGluAlaIleuLys	770
Db	2224	GACCTAAAGGGAGGATATATGGGATTAATGGAGTAAATGATCTATTGTGAGGCTTGAAA	2283
QY	771	HisProLysCysLeuLeuGluSerLeuLysArgLysArgCysCysGlyLeuThrHisAlaCys	790
Db	2284	CACCCAGAGTGAATTAACCTACAGACTCTCAGGGCTGGAACTTGGAACTTAACCTGATTTGGT	2344
QY	791	TyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAla	810
Db	2344	TGCTCAATTAATATCTAATGCTCTCATCGAAGGCCAGAGCTGATATTTCTGAACTGTCA	2403
QY	811	GlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaIleArgValSerGln	830
Db	2404	ACCAATTAATCTGTGGATGATGAGATGAGCTTTGTGTGTGGGCTTAAAGATCCAAAG	2463
QY	831	CysAlaIleGlnLysLeuIleLeuGluLysArgCysGlyIleThrAlaThrGlyCysGlnSer	850
Db	2464	TGTTATCTTAAGAGACTGCTCTTAAGAGCTGTGTCTCACAGAGCTGGCTGTAGAT	2523
QY	851	LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisIleuCysLeuSerAsnAsnSer	870
Db	2524	CTTCTTGGCTGCTCATCAGCAATTAAGAAGCTGAACACATTTGTGCTTGAGACAATGTC	2583
QY	871	LeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu	890
Db	2584	TTGGGTATGGTGGAGTAAAGCTTAATGATGATGCGCCGCAACATGCAATGATCTGTG	2643
QY	891	GlnArgLeuMetLeuAsnGlnCysHisIleuAspThrAlaGlyCysGlyPheLeuAlaLeu	910
Db	2644	AAGAGCCTTGTGCTGAGGCGTGTGCCATTTCACTTCACTTACAGCAATGATTTGTCAACT	2703
QY	911	AlaLeuMetGlyAsnSerTrpLeuThrHisIleuSerLeuSerMetAsnProValGluAsp	930
Db	2704	TCTCTTCAACAAACAAGAGCTGACGATCTGATCTTAAGATCAAACTGGCTACAAAGC	2763
QY	931	AsnGlyValIlybLeuLeuCysGluValMetArgLysProSerCysHisIleuGlnAspLeu	950
Db	2764	AATGAGATGAAGCTTCTGTGATGATCTTTTGGGCAATCAAGCTGATATCTTCAGACATTTG	2823
QY	951	GluLeuValLysCysHisIleuThrAlaAlaCysCysGlnSerLeuSerCysValIleSer	970
Db	2824	GAATTGATGGGCTGTGTTCTCACTAATGCAAGTGTCTGATCTGTGCTTCTGTATTTTG	2883
QY	971	ArgSerArgHisLeuLysSerLeuAspLeuThrArgAsnAlaIleuGlyAspGlyVal	990
Db	2884	AATAACCCAAACCTGAGAGAGCTGACCTTGGGAAACAACGATTTGCAGAGATGATGAGATG	2943
QY	991	AlaAlaIleuCysGluGlyLeuLysGlnLysAsnSerValIleuThrArgLeuGlyLeuLys	1010
Db	2944	AAATATCTGTGTGATGCTTTGAGATATCCAAATCTTAATCAATTCAGAGGCTGGGTTGGAA	3003
QY	1011	AlaCysGlyLeuThrSerArgCysCysGluAlaIleuSerLeuAlaIleuSerCysAsnArg	1030
Db	3004	TACTGTGTGTGACATCTCTCTGCTGCAAAATCTCTCTGCTCTTAATCTGCAACAA	3063
QY	1031	HisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeu	1050
Db	3064	AGACTGATAAATGAATCTGACACAGAAATCTTAAGATATGAAGAAATGTGAAGTTA	3123
QY	1051	CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGln	1070
Db	3124	TATAAAGCTTGAAGTCTCTTAAGTGAATCAACAAGTTCTAAGGTTGTGCAAAAGGCA	3183
QY	1071	TyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLysProArgValVal	1090
Db	3184	TTTGTATGGAAGCCCAAGACCTGTGAACTGTGGAGATTTAGCATCCACACTTAATC	3243
QY	1091	IleAspGlySerTrpHisSerPheAspThrAsp	1102
Db	3244	ATTAAAGCAAGTGTAACTATCATTAATGAAGAAGAT	3279

RESULT 15

Qy	540	TrypMetLysArgPheLeuPheGluLeuValSerGluAspValArgArgProLeuGluVal	559
Dp	1561	TTTTGGGGGCTTTTCTAACTGGCTTTTAAATTAAGAAAGAAAGAAACTGGATGGC	1622
Qy	560	LeuLeuGluCysProValProLeuGluValLysGlnLysLeuLeuHisIleTrpValSerLeu	579
Dp	1621	TTTTTTGGCTTCCAACTGCTCCCAAGATATTAAGACAAATTCACAGTGGCTTAAGAC	1688
Qy	580	LeuGluGlnGlnProAspAlaThrThrProGluAspThrLeuAspAlaPheHisCysLeu	599
Dp	1681	TTAAGGGAGCGTGGCAATCTCTCAGAGGACGGGATTCCTTGGCGATTTTAACTGTCTC	1740
Qy	600	PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp	619
Dp	1741	TTTGAATAAGCAGGAATCTGCCCTTGTGAAGCAGGAGTAATCTCTCCAGAAACTAAC	1800
Qy	620	LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro	639
Dp	1801	TTTCAATATTAATTAAGACACGTGGACTGTGGTGTTTCTGCTACTGTTTAAATACGTCC	1866
Qy	640	TyrIleuArgLysIleArgValAspValLysGluIlePheProArgAspGluSerAlaGlu	659
Dp	1861	AGCTTGAAGAAACTGTGTTTTCCGTTCAAAATGCTTTAAGAAAGAGATGAACACAGC	1922
Qy	660	AlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluIleTrpIu	679
Dp	1921	TCT-----ACGTGGATTAACGCTTCATC-----TGTGGCAT	1953
Qy	680	AspPheCysSerMetLeuGluYThrHisProHisIleuArgGlnLeuAspLeuGluYSerSer	699
Dp	1954	CACATCTGCTGTGCTCAACCAAGGGGACCTCAGAAAGCTCAGGTGAGAGAC	2013
Qy	700	IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysValLysLeuGlnHisProThrCysLys	719
Dp	2014	ACCGTCAGAGTGCACCTTGTGTACCTGTGTAAACAGTGAAGCATCCAGCGTGTGC	2073
Qy	720	IleGlnThrLeuMetPheArgAspAlaGlnIleThrProGluValGlnHisLeuTrpArg	739
Dp	2074	CTTCAGAAAGCTTGAGTAATTAATTAACCTTTCCTTTTGGCCAGAGTGTTCTGCTCTTGA	2133
Qy	740	IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluGluYThrHisLeuLysGlu	759
Dp	2134	GTGCTCTTTTATCAGCCAGACTGTAAATAACCTGACCTTCACCTCAGAAATCTCTGCT	2193
Qy	760	GluAspValArgMetAlaCysGluLysIleLeuLysHisProLysCysLeuLeuGluSerLeu	779
Dp	2194	GATACATCAAGGTCCCTCTGTGATGCTCTTGAACATCAACCA-----	2233
Qy	780	ArgLeuAspCysCysGluLeuThrHisAlaCysTyrLeuLysHisSerGlnIleLeuThr	799
Dp	2232	-----	2233
Qy	800	ThrSerProSerLeuLysSerLeuSerLeuAlaGluAlaAsnLysValThrAspGlnGluVal	819
Dp	2233	-----GAGGCCAAC-----	2241
Qy	820	MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu	839
Dp	2242	-----GTCAAAAGACTACCGCTGGTA	2266
Qy	840	AspCysGluYIleThrAlaThrGluCysGlnSerLeuAlaSerAlaLeuValSerAsnArg	859
Dp	2263	AATGTGCACCTGTACACCATTTGATGTGAAGTCTGTGGCTCTTAACCAACAAG	2322
Qy	860	SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGluYAsnGluGluValAsnLeuLeu	879
Dp	2323	AAGCTGAGTATCTGAATGTATCTCGCAACACAGTTA---GACACAGGGGTGCCCTTTTG	2379
Qy	880	CysArgSerMetArgLeuProHisCysSerLeuGlnAlaGluMetLeuAsnGlnCysHis	899
Dp	2380	TGTGAAGCCCTGTGCAGGCCAGACACGGTCTGTGTATACCTGATGTGGCTTTCTGGCAC	2433

QY	LeuSepThrAlaGLyCyGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr	919
Db	CTCAGCAGACAGCTGCTGGCAATCATCTCTGAAATGCTTCTTCGCGTAAACAAGCCGTGGC	2499
QY	HisLeuSerLeuSerMetLeuAsnProValGluAspAsnGlyValAllysLeuLeuCyGlyGluVal	939
Db	2500 TATCTAGACCTCAGTGGCCAAATGTCTCTGAAGACGAAAGGACTGAAAACTCTCTGCGAGGCC	2555
QY	MetArgGluProSerCyGhiLeuGlnAspLeuGluLeuValIysCyGhiLeuThrAla	959
Db	2560 TTGAACACATCCGAGCTGCTGCCTGGATTCACTGTGTTTGGTAAATATTTTATCATCTCT	2615
QY	AlaCyCyGlyGlnSerLeuSerCyValIleSerThrSerArgHisLeuIysSerLeuAsp	979
Db	2620 GCTGGCTGTGAAGACCTTGCTCTGCTCTCTCATCAGCATTCMAACCTGAAGATTCTGCA	2677
QY	LeuThrAspAsnAlaLeuGlyAspPolYgIyValAlaAlaLeuCyGlyGluIysLeuIysGln	999
Db	2680 ATTGGGTGCATATGAATATCGAGAGATGTGGGTGTGCGAGCTGTGTGTCGGGCTCTGACGAT	2738
QY	LysAsnSerValLeuThrArgLeuGlyLeuIysAlaCyGlyIysLeuThrSerAspCyGly	1015
Db	2740 ACGGATTGCCCTTGAAGATTCCTGGGTGGAGAAATGGGTAAACGAGCACCCTGCTGT	2795
QY	GluAlaLeuSerLeuAlaLeuSerCyAsnAspArgHisLeuThrSerLeuAsnLeuValGln	1035
Db	2800 AAGATCTTCGGGCTGCTTCTCACTCGATGAGAACCTTCGACGACCTCAACTGACTTG	2855
QY	AsnAspPheSerProIysGlyMetMetIysLeuCySerAlaPheAlaCyAspProThrSer	1055
Db	2860 AACAACCTTGACACACAGGAGGTGTGTACTCTGTGAGCGCCCTGACACACCAAGAGT	2915
QY	AsnLeuGlnIleIleGlyLeuTrpIysTrpGlnTrpProValGlnIleArgIysLeuLeu	1075
Db	2920 GCCCTGACGGGTCTCCGGCTGAGAAAACATGATTTTGTATGAGAAACCCAGCACTTCTG	2975
QY	GluGluValGlnLeuLeuLeuProArgValValIleAsp	1092
Db	2980 ACGGCTGAGAGAGAGAAATCTTAACCTGACCATCAAGATGACTGACACAAATCA	3038
QY	GlySerTrpHisSerPheAspGluAspAspArgHisIlys	1105
Db	3040 AGGGTAGAGATCTGATTGCCAGGAACCTGG	3065
QY	IleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCyAlaLeuLeuTrpGly	1122
Db	3070 ---GCTCTGACTCGAACAACCTGCAAAAGGACGAGGACTGGGAC---CGTTACTTATCATGAC	3123
QY	MetAsnProGluGlnIlyIysArgValSerLeu	1136
Db	3124 ACTGCACCCGAGAGATTAACAATTCATTTCAACTCTC	3156

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Job time : 1762 secs

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